

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 18:18:32 ; Search time 204 Seconds
(without alignments)
7275.015 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 907

Sequence: 1 ggagcttggaagtcacacg.....gtgagactccatccacaca 907

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database: Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/prodata/1/ina/PCUTS.COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905.4	99.8	12445	US-09-949-016-14632	Sequence 14632, A
2	905.4	99.8	21691	US-09-949-016-15748	Sequence 15748, A
3	601.6	66.3	1154	US-09-799-451-704	Sequence 204, App
4	500	55.1	500	US-09-276-531-73	Sequence 73, Appl
5	211.8	23.4	160759	US-09-949-016-16514	Sequence 16514, A
6	211.8	23.3	23533	US-09-949-016-15377	Sequence 15377, A
7	210.6	23.2	36148	US-09-949-016-12969	Sequence 12969, A
8	210.6	23.2	64813	US-09-949-016-11957	Sequence 11957, A
9	210.6	23.2	70131	US-09-949-016-16064	Sequence 16064, A
10	210.4	23.2	63187	US-09-949-016-12682	Sequence 12682, A
11	210.4	23.2	63187	US-09-949-016-16288	Sequence 16288, A
12	209.2	23.1	35678	US-09-949-016-12786	Sequence 12786, A
13	209.2	23.1	35678	US-09-949-016-16757	Sequence 16757, A
14	209.2	23.1	35678	US-09-949-016-16758	Sequence 16758, A
15	209.2	23.1	58361	US-09-949-016-16755	Sequence 16755, A
16	209.2	23.1	58361	US-09-949-016-16756	Sequence 16756, A
17	209.2	23.1	59065	US-09-813-817-3	Sequence 3, Appl1
18	209.2	23.1	59065	US-09-978-197-3	Sequence 3, Appl1
19	209.2	23.1	59065	US-10-135-686-3	Sequence 3, Appl1
20	209.2	23.1	71815	US-09-949-016-12501	Sequence 12501, A
21	209.2	23.0	125672	US-09-949-016-16956	Sequence 16956, A
22	208.8	23.0	601	US-09-949-016-121405	Sequence 121405, A
23	208.8	23.0	48691	US-09-949-016-16308	Sequence 16308, A
24	208.6	23.0	12708	US-09-949-016-13216	Sequence 13216, A
25	208.4	23.0	601	US-09-949-016-163069	Sequence 163069, A
26	208.4	23.0	601	US-09-949-016-163070	Sequence 163070, A
27	208.2	23.0	107941	US-09-949-016-14206	Sequence 14206, A
28	208.2	23.0	109378	US-09-949-016-12391	Sequence 12391, A
29	207.8	22.9	164061	US-09-949-016-17422	Sequence 17422, A
30	207.8	22.9	81201	US-09-949-016-14891	Sequence 14891, A
31	207.8	22.9	94855	US-09-949-016-12264	Sequence 12264, A
32	207.6	22.9	194889	US-09-949-016-15654	Sequence 15654, A
33	207.6	22.9	55886	US-09-949-016-15129	Sequence 15129, A
34	207.4	22.8	54161	US-09-949-016-11905	Sequence 11905, A
35	207.2	22.8	601	US-09-949-016-96561	Sequence 96561, A
36	207.2	22.8	601	US-09-949-016-96827	Sequence 96827, A
37	207.2	22.8	601	US-09-949-016-97093	Sequence 97093, A
38	207.2	22.8	601	US-09-949-016-97359	Sequence 97359, A
39	207.2	22.8	601	US-09-949-016-97625	Sequence 97625, A
40	207.2	22.8	601	US-09-949-016-97891	Sequence 97891, A
41	207.2	22.8	601	US-09-949-016-98157	Sequence 98157, A
42	207.2	22.8	601	US-09-949-016-98423	Sequence 98423, A
43	207.2	22.8	601	US-09-949-016-98689	Sequence 98689, A
44	207.2	22.8	601	US-09-949-016-98955	Sequence 98955, A
45	207.2	22.8	601	US-09-949-016-99221	Sequence 99221, A
46	207.2	22.8	601	US-09-949-016-99487	Sequence 99487, A
47	207.2	22.8	601	US-09-949-016-99753	Sequence 99753, A
48	207.2	22.8	601	US-09-949-016-100019	Sequence 100019, A
49	207.2	22.8	601	US-09-949-016-100285	Sequence 100285, A
50	207.2	22.8	601	US-09-949-016-100511	Sequence 100511, A
51	207.2	22.8	601	US-09-949-016-100817	Sequence 100817, A
52	207.2	22.8	601	US-09-949-016-101121	Sequence 101121, A
53	207.2	22.8	601	US-09-949-016-101387	Sequence 101387, A
54	207.2	22.8	601	US-09-949-016-101653	Sequence 101653, A
55	207.2	22.8	601	US-09-949-016-101919	Sequence 101919, A
56	207.2	22.8	601	US-09-949-016-102339	Sequence 102339, A
57	207.2	22.8	601	US-09-949-016-102479	Sequence 102479, A
58	207.2	22.8	44715	US-09-949-016-16353	Sequence 16353, A
59	207.2	22.8	38575	US-09-949-016-17304	Sequence 17304, A
60	207.2	22.8	63804	US-09-949-016-15200	Sequence 15200, A
61	207.2	22.8	119153	US-09-949-016-12378	Sequence 12378, A
62	206.8	22.8	152582	US-09-949-016-163071	Sequence 163071, A
63	206.8	22.8	152582	US-09-949-016-12086	Sequence 12086, A
64	206.8	22.8	152582	US-09-949-016-17390	Sequence 17390, A
65	206.8	22.8	152583	US-09-949-016-13029	Sequence 13029, A
66	206.6	22.8	601	US-09-949-016-196297	Sequence 196297, A
67	206.6	22.8	601	US-09-949-016-16250	Sequence 16250, A
68	206.6	22.8	26831	US-09-949-016-38425	Sequence 38425, A
69	206.2	22.7	601	US-09-949-016-161039	Sequence 161039, A
70	206.2	22.7	601	US-09-949-016-176177	Sequence 176177, A
71	206.2	22.7	601	US-09-949-016-176230	Sequence 176230, A
72	206.2	22.7	601	US-09-949-016-176288	Sequence 176288, A
73	206.2	22.7	601	US-09-949-016-176306	Sequence 176306, A
74	206.2	22.7	39231	US-09-949-016-16533	Sequence 16533, A
75	206.2	22.7	17612	US-09-949-016-15061	Sequence 15061, A
76	206	22.7	23781	US-09-949-016-13446	Sequence 13446, A
77	206	22.7	42574	US-09-949-016-17525	Sequence 17525, A
78	206	22.7	393753	US-09-949-016-14574	Sequence 14574, A
79	206	22.7	393753	US-09-949-016-14575	Sequence 14575, A
80	206	22.7	670689	US-09-949-016-12505	Sequence 12505, A
81	206	22.7	670689	US-09-949-016-14551	Sequence 14551, A
82	206	22.7	818128	US-09-949-016-14550	Sequence 14550, A
83	206	22.7	818128	US-09-949-016-14548	Sequence 14548, A
84	206	22.7	818128	US-09-949-016-14549	Sequence 14549, A
85	206	22.7	818128	US-09-949-016-14554	Sequence 14554, A
86	206	22.7	818128	US-09-949-016-14555	Sequence 14555, A
87	206	22.7	818128	US-09-949-016-14556	Sequence 14556, A
88	206	22.7	818128	US-09-949-016-14557	Sequence 14557, A
89	206	22.7	818128	US-09-949-016-14558	Sequence 14558, A
90	206	22.7	818128	US-09-949-016-14559	Sequence 14559, A
91	206	22.7	818128	US-09-949-016-14560	Sequence 14560, A
92	206	22.7	818128	US-09-949-016-14561	Sequence 14561, A
93	206	22.7	818128	US-09-949-016-14562	Sequence 14562, A
94	206	22.7	818128	US-09-949-016-14564	Sequence 14564, A
95	206	22.7	818128	US-09-949-016-14565	Sequence 14565, A
96	206	22.7	818128	US-09-949-016-14566	Sequence 14566, A
97	206	22.7	818128	US-09-949-016-14567	Sequence 14567, A
98	206	22.7	818128	US-09-949-016-14568	Sequence 14568, A
99	206	22.7	818128	US-09-949-016-14569	Sequence 14569, A
100	206	22.7	818128	US-09-949-016-14570	Sequence 14570, A

101	206	22.7	818128	4	US-09-949-016-14565	Sequence 14565, A
102	206	22.7	818128	4	US-09-949-016-14566	Sequence 14566, A
103	206	22.7	818128	4	US-09-949-016-14567	Sequence 14567, A
104	205.8	22.7	118192	4	US-09-949-016-17084	Sequence 17084, A
105	205.8	22.7	43550	4	US-09-949-016-12400	Sequence 12400, A
106	205.8	22.7	43555	4	US-09-949-016-13993	Sequence 13993, A
107	205.8	22.7	144596	4	US-09-949-016-11749	Sequence 11749, A
108	205.8	22.7	144596	4	US-09-949-016-11749	Sequence 11749, A
109	205.6	22.7	601	4	US-09-949-016-17835	Sequence 17835, A
110	205.6	22.7	601	4	US-09-949-016-41705	Sequence 41705, A
111	205.6	22.7	601	4	US-09-949-016-96560	Sequence 96560, A
112	205.6	22.7	601	4	US-09-949-016-96826	Sequence 96826, A
113	205.6	22.7	601	4	US-09-949-016-97092	Sequence 97092, A
114	205.6	22.7	601	4	US-09-949-016-97358	Sequence 97358, A
115	205.6	22.7	601	4	US-09-949-016-97624	Sequence 97624, A
116	205.6	22.7	601	4	US-09-949-016-97890	Sequence 97890, A
117	205.6	22.7	601	4	US-09-949-016-98156	Sequence 98156, A
118	205.6	22.7	601	4	US-09-949-016-98422	Sequence 98422, A
119	205.6	22.7	601	4	US-09-949-016-98688	Sequence 98688, A
120	205.6	22.7	601	4	US-09-949-016-98954	Sequence 98954, A
121	205.6	22.7	601	4	US-09-949-016-99220	Sequence 99220, A
122	205.6	22.7	601	4	US-09-949-016-99486	Sequence 99486, A
123	205.6	22.7	601	4	US-09-949-016-99752	Sequence 99752, A
124	205.6	22.7	601	4	US-09-949-016-100018	Sequence 100018, A
125	205.6	22.7	601	4	US-09-949-016-100284	Sequence 100284, A
126	205.6	22.7	601	4	US-09-949-016-100550	Sequence 100550, A
127	205.6	22.7	601	4	US-09-949-016-100816	Sequence 100816, A
128	205.6	22.7	601	4	US-09-949-016-101120	Sequence 101120, A
129	205.6	22.7	601	4	US-09-949-016-101386	Sequence 101386, A
130	205.6	22.7	601	4	US-09-949-016-101652	Sequence 101652, A
131	205.6	22.7	601	4	US-09-949-016-102338	Sequence 102338, A
132	205.6	22.7	601	4	US-09-949-016-102478	Sequence 102478, A
133	205.6	22.7	601	4	US-09-949-016-119486	Sequence 119486, A
134	205.6	22.7	26852	4	US-09-949-016-12736	Sequence 12736, A
135	205.6	22.7	26852	4	US-09-949-016-15823	Sequence 15823, A
136	205.6	22.7	193169	4	US-09-949-016-15091	Sequence 15091, A
137	205.6	22.7	47284	4	US-09-949-016-17029	Sequence 17029, A
138	205.4	22.6	56516	2	US-08-996-306-1	Sequence 1, Appl1
139	205.4	22.6	56516	3	US-09-338-907-1	Sequence 1, Appl1
140	205.4	22.6	56516	3	US-09-338-907-1	Sequence 1, Appl1
141	205.4	22.6	56520	3	US-09-338-907-1	Sequence 179, App
142	205.4	22.6	56520	3	US-09-218-207-179	Sequence 179, App
143	205.4	22.6	56520	3	US-09-218-207-179	Sequence 149191, A
144	205.2	22.6	601	4	US-09-949-016-149191	Sequence 149191, A
145	205.2	22.6	8345	4	US-09-949-016-16833	Sequence 16833, A
146	205.2	22.6	12013	4	US-09-949-016-15938	Sequence 15938, A
147	205.2	22.6	12013	4	US-09-949-016-15939	Sequence 15939, A
148	205.2	22.6	42373	4	US-09-949-016-16438	Sequence 16438, A
149	205.2	22.6	601	4	US-09-949-016-184743	Sequence 184743, A
150	204.8	22.6	601	4	US-09-949-016-148190	Sequence 148190, A
151	204.8	22.6	601	4	US-09-949-016-149192	Sequence 149192, A
152	204.8	22.6	601	4	US-09-949-016-149195	Sequence 149195, A
153	204.8	22.6	601	4	US-09-949-016-149197	Sequence 149197, A
154	204.8	22.6	74804	4	US-09-949-016-15118	Sequence 15118, A
155	204.8	22.6	601	4	US-09-949-016-33416	Sequence 33416, A
156	204.6	22.6	601	4	US-09-949-016-41051	Sequence 41051, A
157	204.6	22.6	42954	4	US-09-949-016-17123	Sequence 17123, A
158	204.6	22.6	42954	4	US-09-949-016-17124	Sequence 17124, A
159	204.6	22.6	66055	4	US-09-949-016-13292	Sequence 13292, A
160	204.6	22.6	88950	4	US-09-949-016-17150	Sequence 17150, A
161	204.6	22.6	88950	4	US-09-949-016-17150	Sequence 17150, A
162	204.4	22.5	10029	4	US-09-949-016-11846	Sequence 11846, A
163	204.4	22.5	10029	4	US-09-949-016-16140	Sequence 16140, A
164	204.4	22.5	104520	4	US-09-949-016-13303	Sequence 13303, A
165	204.4	22.5	126029	4	US-09-949-016-14731	Sequence 14731, A
166	204.4	22.5	144158	4	US-09-949-016-11755	Sequence 11755, A
167	204.4	22.5	144158	4	US-09-949-016-12936	Sequence 12936, A
168	204.4	22.5	363032	4	US-09-949-016-12936	Sequence 12936, A
169	204.4	22.5	363032	4	US-09-949-016-15754	Sequence 15754, A
170	204.2	22.5	4736	4	US-09-526-193A-15	Sequence 15, Appl1
171	204.2	22.5	98864	4	US-09-949-016-15403	Sequence 15403, A
172	204	22.5	601	4	US-09-949-016-120817	Sequence 120817, A
173	204	22.5	7561	4	US-09-949-016-11816	Sequence 11816, A
174	204	22.5	7562	4	US-09-949-016-13895	Sequence 13895, A
175	204	22.5	28556	4	US-09-949-016-13064	Sequence 13064, A
176	204	22.5	40037	4	US-09-949-016-12715	Sequence 12715, A
177	204	22.5	43335	4	US-09-949-016-12905	Sequence 12905, A
178	204	22.5	189560	4	US-09-949-016-11202	Sequence 11202, A
179	204	22.5	421118	4	US-09-949-016-12927	Sequence 16297, A
180	203.8	22.5	99500	3	US-09-798-096-10	Sequence 10, Appl1
181	203.8	22.5	601	4	US-09-949-016-13106	Sequence 163106, A
182	203.6	22.4	25122	4	US-09-949-016-16382	Sequence 16382, A
183	203.6	22.4	175265	4	US-09-949-016-15089	Sequence 16089, A
184	203.6	22.4	194393	4	US-09-949-016-14172	Sequence 14172, A
185	203.4	22.4	601	4	US-09-949-016-33415	Sequence 33415, A
186	203.4	22.4	601	4	US-09-949-016-41050	Sequence 41050, A
187	203.4	22.4	30456	4	US-09-949-016-14213	Sequence 14213, A
188	203.4	22.4	44439	4	US-09-949-016-11102	Sequence 17102, A
189	203.4	22.4	47727	4	US-09-949-016-12904	Sequence 12904, A
190	203.4	22.4	62128	4	US-09-949-016-12539	Sequence 12539, A
191	203.4	22.4	112114	4	US-09-949-016-17292	Sequence 17292, A
192	203.4	22.4	154605	4	US-09-949-016-11894	Sequence 11894, A
193	203.4	22.4	227750	4	US-09-949-016-11715	Sequence 11715, A
194	203.2	22.4	98439	4	US-09-949-016-13597	Sequence 13597, A
195	203.2	22.4	136264	4	US-09-949-016-13766	Sequence 13766, A
196	203.2	22.4	136265	4	US-09-949-016-13001	Sequence 13001, A
197	203.2	22.4	178883	4	US-09-949-016-12733	Sequence 12733, A
198	203.2	22.4	178884	4	US-09-949-016-13039	Sequence 13039, A
199	203.2	22.4	236474	4	US-09-949-016-13418	Sequence 13418, A
200	203	22.4	601	4	US-09-949-016-33417	Sequence 33417, A
201	203	22.4	601	4	US-09-949-016-33418	Sequence 33418, A
202	203	22.4	601	4	US-09-949-016-33419	Sequence 33419, A
203	203	22.4	601	4	US-09-949-016-41052	Sequence 41052, A
204	203	22.4	601	4	US-09-949-016-41053	Sequence 41053, A
205	203	22.4	601	4	US-09-949-016-41054	Sequence 41054, A
206	203	22.4	40742	4	US-09-949-016-11751	Sequence 11751, A
207	203	22.4	40747	4	US-09-949-016-13097	Sequence 13097, A
208	203	22.4	46085	4	US-09-949-016-13547	Sequence 13547, A
209	203	22.4	46085	4	US-09-949-016-13548	Sequence 13548, A
210	203	22.4	56441	4	US-09-949-016-15174	Sequence 15174, A
211	203	22.4	56441	4	US-09-949-016-15175	Sequence 15175, A
212	203	22.4	69709	4	US-09-949-016-15784	Sequence 15784, A
213	203	22.4	107458	4	US-09-949-016-13687	Sequence 13687, A
214	203	22.4	114793	4	US-10-148-806-3	Sequence 3, Appl1
215	203	22.4	123663	4	US-09-949-016-14202	Sequence 14202, A
216	203	22.4	146639	4	US-09-949-016-12449	Sequence 12449, A
217	203	22.4	276337	4	US-09-949-016-17504	Sequence 17504, A
218	202.8	22.4	27667	4	US-09-841-159-5	Sequence 5, Appl1
219	202.8	22.4	40168	4	US-09-949-016-11225	Sequence 11225, A
220	202.8	22.4	51508	4	US-09-949-016-16681	Sequence 16681, A
221	202.8	22.4	93510	4	US-09-949-016-15095	Sequence 15095, A
222	202.6	22.3	601	4	US-09-949-016-23936	Sequence 23936, A
223	202.6	22.3	601	4	US-09-949-016-139600	Sequence 139600, A
224	202.6	22.3	601	4	US-09-949-016-18623	Sequence 18623, A
225	202.6	22.3	23532	4	US-09-949-016-16270	Sequence 16270, A
226	202.6	22.3	45138	4	US-09-949-016-13027	Sequence 13027, A
227	202.6	22.3	68392	4	US-09-949-016-13626	Sequence 13626, A
228	202.6	22.3	69763	4	US-09-949-016-12584	Sequence 12584, A
229	202.6	22.3	601	4	US-09-949-016-17479	Sequence 17479, A
230	202.4	22.3	601	4	US-09-949-016-131425	Sequence 191425, A
231	202.4	22.3	26007	4	US-09-949-016-17222	Sequence 17222, A
232	202.4	22.3	31113	4	US-09-949-016-15960	Sequence 16960, A
233	202.4	22.3	44447	4	US-09-949-016-12018	Sequence 12018, A
234	202.4	22.3	44447	4	US-09-949-016-11101	Sequence 11101, A
235	202.4	22.3	62354	4	US-09-949-016-11188	Sequence 16188, A
236	202.4	22.3	63330	4	US-09-949-016-12270	Sequence 12270, A
237	202.4	22.3	109690	4	US-09-949-016-13525	Sequence 13525, A
238	202.4	22.3	115635	4	US-09-949-016-12298	Sequence 12298, A
239	202.4	22.3	144422	4	US-09-949-016-13316	Sequence 15316, A
240	202.4	22.3	247599	4	US-09-949-016-17590	Sequence 17590, A
241	202.2	22.3	9365	3	US-09-608-285A-8	Sequence 8, Appl1
242	202.2	22.3	9365	3	US-09-350-835B-8	Sequence 8, Appl1
243	202.2	22.3	9365	3	US-09-370-265-8	Sequence 8, Appl1
244	202.2	22.3	9365	3	US-09-557-800C-8	Sequence 8, Appl1
245	202.2	22.3	9365	4	US-09-370-622A-8	Sequence 42, Appl1
246	202.2	22.3	14747	3	US-09-608-285A-42	Sequence 42, Appl1

C 247	202.2	22.3	14747	4	US-09-557-800C-42	Sequence 42, Appl	320	201	22.2	108441	4	US-09-949-016-14090	Sequence 14090, A
C 248	202.2	22.3	15977	3	US-09-608-285A-59	Sequence 59, Appl	321	201	22.2	167708	4	US-09-949-016-14423	Sequence 16423, A
C 249	202.2	22.3	24593	4	US-09-949-016-13333	Sequence 13433, A	322	200.8	22.1	4421	2	US-08-257-963B-9	Sequence 9, Appl1
C 250	202.2	22.3	30843	4	US-09-949-016-14487	Sequence 14487, A	323	200.8	22.1	4421	3	US-08-367-841A-9	Sequence 9, Appl1
C 251	202.2	22.3	91831	4	US-09-949-016-13694	Sequence 13694, A	324	200.8	22.1	4421	5	PCR-US95-07201-9	Sequence 6, Appl1
C 252	202.2	22.3	107897	4	US-09-949-016-13118	Sequence 13118, A	325	200.8	22.1	11729	4	US-09-949-016-13247	Sequence 13247, A
C 253	202.2	22.3	107937	4	US-09-949-016-17192	Sequence 17192, A	326	200.8	22.1	11729	4	US-09-949-016-13123	Sequence 13123, A
C 254	202.2	22.3	116425	4	US-09-949-016-11809	Sequence 11809, A	327	200.8	22.1	13445	4	US-09-949-016-15152	Sequence 13512, A
C 255	202.2	22.3	235452	4	US-09-949-016-13675	Sequence 13675, A	328	200.8	22.1	13445	4	US-09-949-016-11235	Sequence 17255, A
C 256	202.2	22.3	601	4	US-09-949-016-33414	Sequence 33414, A	329	200.8	22.1	95122	4	US-09-949-016-11235	Sequence 16926, A
C 257	202.2	22.3	601	4	US-09-949-016-41049	Sequence 41049, A	330	200.8	22.1	107820	4	US-09-792-616-1	Sequence 1, Appl1
C 258	202.2	22.3	168104	4	US-09-949-016-12926	Sequence 12026, A	331	200.8	22.1	319608	4	US-09-539-333D-1	Sequence 1, Appl1
C 259	202.2	22.3	168105	4	US-09-949-016-16554	Sequence 16554, A	332	200.8	22.1	319608	4	US-09-679-409-1	Sequence 16045, A
C 260	201.8	22.2	27783	4	US-09-949-016-16736	Sequence 16736, A	333	200.6	22.1	39601	4	US-09-949-016-15045	Sequence 3, Appl1
C 261	201.8	22.2	50518	4	US-09-949-016-12315	Sequence 12315, A	334	200.6	22.1	55827	3	US-09-813-133A-3	Sequence 3, Appl1
C 262	201.8	22.2	51110	4	US-09-949-016-12069	Sequence 12069, A	335	200.6	22.1	55827	4	US-10-212-877-3	Sequence 15118, A
C 263	201.8	22.2	51111	4	US-09-949-016-15724	Sequence 15724, A	336	200.6	22.1	74804	4	US-09-949-016-15964	Sequence 15964, A
C 264	201.8	22.2	55551	4	US-09-949-016-12030	Sequence 12030, A	337	200.6	22.1	103987	4	US-09-949-016-12513	Sequence 12513, A
C 265	201.8	22.2	58782	4	US-09-949-016-16851	Sequence 16851, A	338	200.6	22.1	103987	4	US-09-949-016-17050	Sequence 17050, A
C 266	201.8	22.2	60417	4	US-09-949-016-13312	Sequence 13312, A	339	200.6	22.1	103988	4	US-09-949-016-1561	Sequence 17562, A
C 267	201.8	22.2	60572	4	US-09-949-016-12702	Sequence 12702, A	340	200.6	22.1	113379	4	US-09-949-016-17562	Sequence 15602, A
C 268	201.8	22.2	60592	4	US-09-949-016-13741	Sequence 13741, A	341	200.6	22.1	113379	4	US-09-949-016-15640	Sequence 15640, A
C 269	201.8	22.2	84763	4	US-09-949-016-11919	Sequence 11919, A	342	200.6	22.1	113379	4	US-09-949-016-12268	Sequence 12268, A
C 270	201.8	22.2	84763	4	US-09-949-016-13914	Sequence 13914, A	343	200.4	22.1	13985	4	US-09-949-016-15602	Sequence 15602, A
C 271	201.8	22.2	131332	4	US-09-949-016-15335	Sequence 15335, A	344	200.4	22.1	30636	4	US-09-949-016-12268	Sequence 16508, A
C 272	201.8	22.2	131332	4	US-09-949-016-16513	Sequence 16513, A	345	200.4	22.1	30636	4	US-09-949-016-15088	Sequence 17188, A
C 273	201.8	22.2	234288	4	US-09-949-016-17272	Sequence 17272, A	346	200.4	22.1	30337	4	US-09-949-016-17188	Sequence 16874, A
C 274	201.8	22.2	285986	4	US-09-949-016-12878	Sequence 12878, A	347	200.4	22.1	31797	4	US-09-949-016-11864	Sequence 12884, A
C 275	201.8	22.2	288031	4	US-09-949-016-14864	Sequence 14864, A	348	200.4	22.1	31875	4	US-09-949-016-1864	Sequence 15857, A
C 276	201.6	22.2	29614	4	US-09-949-016-15683	Sequence 15683, A	349	200.4	22.1	52824	4	US-09-949-016-11516	Sequence 12116, A
C 277	201.6	22.2	29614	4	US-09-949-016-12590	Sequence 12590, A	350	200.4	22.1	52824	4	US-09-949-016-12513	Sequence 12513, A
C 278	201.6	22.2	46339	4	US-09-949-016-12526	Sequence 12526, A	351	200.4	22.1	103887	4	US-09-949-016-17050	Sequence 17050, A
C 279	201.6	22.2	46339	4	US-09-949-016-13267	Sequence 13267, A	352	200.4	22.1	103887	4	US-09-949-016-112169	Sequence 12169, A
C 280	201.6	22.2	50959	4	US-09-949-016-16659	Sequence 16659, A	353	200.2	22.1	601	4	US-09-949-016-12169	Sequence 12169, A
C 281	201.6	22.2	246240	2	US-08-724-394A-20	Sequence 20, Appl	354	200.2	22.1	601	4	US-09-949-016-127564	Sequence 127564, A
C 282	201.6	22.2	246240	2	US-08-724-394A-21	Sequence 21, Appl	355	200.2	22.1	601	4	US-09-949-016-167008	Sequence 167008, A
C 283	201.6	22.2	246240	2	US-08-724-394A-22	Sequence 22, Appl	356	200.2	22.1	601	4	US-09-949-016-168914	Sequence 168914, A
C 284	201.4	22.2	246240	2	US-08-724-394A-22	Sequence 22, Appl	357	200.2	22.1	601	4	US-09-949-016-168914	Sequence 168914, A
C 285	201.4	22.2	601	4	US-09-949-016-169981	Sequence 169981, A	358	200.2	22.1	601	4	US-09-949-016-185499	Sequence 185499, A
C 286	201.4	22.2	601	4	US-09-949-016-181571	Sequence 181571, A	359	200.2	22.1	601	4	US-09-949-016-13465	Sequence 13465, A
C 287	201.4	22.2	601	4	US-09-949-016-181572	Sequence 181572, A	360	200.2	22.1	17459	4	US-09-949-016-13465	Sequence 13076, A
C 288	201.4	22.2	15720	4	US-09-949-016-11780	Sequence 11780, A	361	200.2	22.1	28257	4	US-09-949-016-13076	Sequence 12515, A
C 289	201.4	22.2	15739	4	US-09-949-016-14233	Sequence 14233, A	362	200.2	22.1	28257	4	US-09-949-016-13076	Sequence 15338, A
C 290	201.4	22.2	29165	4	US-09-949-016-12340	Sequence 12340, A	363	200.2	22.1	28843	4	US-09-949-016-15338	Sequence 11772, A
C 291	201.4	22.2	29771	4	US-09-949-016-12754	Sequence 12754, A	364	200.2	22.1	61313	4	US-09-949-016-15338	Sequence 15560, A
C 292	201.4	22.2	29771	4	US-09-949-016-13956	Sequence 13956, A	365	200.2	22.1	71574	4	US-09-949-016-15809	Sequence 17149, A
C 293	201.4	22.2	40655	4	US-09-949-016-12032	Sequence 12032, A	366	200.2	22.1	83349	4	US-09-949-016-17149	Sequence 1, Appl1
C 294	201.4	22.2	40655	4	US-09-949-016-15919	Sequence 15919, A	367	200.2	22.1	106746	4	US-09-326-402C-1	Sequence 12, Appl
C 295	201.4	22.2	58593	4	US-09-949-016-12232	Sequence 12232, A	368	200.2	22.1	106746	4	US-09-326-402C-12	Sequence 16356, A
C 296	201.4	22.2	64467	4	US-09-803-671B-3	Sequence 3, Appl1	369	200.2	22.1	114139	4	US-09-949-016-16356	Sequence 13413, A
C 297	201.4	22.2	64467	4	US-10-274-409-3	Sequence 3, Appl1	370	200.2	22.1	114139	4	US-09-949-016-13413	Sequence 16284, A
C 298	201.4	22.2	68529	4	US-09-949-016-12140	Sequence 12140, A	371	200.2	22.1	114139	4	US-09-949-016-16284	Sequence 24898, A
C 299	201.4	22.2	68529	4	US-09-949-016-15671	Sequence 15671, A	372	200.2	22.1	240157	4	US-09-949-016-24898	Sequence 24899, A
C 300	201.2	22.2	32202	4	US-09-949-016-15357	Sequence 15357, A	373	200.2	22.1	601	4	US-09-949-016-33413	Sequence 33413, A
C 301	201.2	22.2	32202	4	US-09-949-016-12140	Sequence 12140, A	374	200.2	22.1	601	4	US-09-949-016-33413	Sequence 41048, A
C 302	201.2	22.2	68529	4	US-09-949-016-15671	Sequence 15671, A	375	200.2	22.1	601	4	US-09-949-016-13413	Sequence 138409, A
C 303	201.2	22.2	79835	4	US-09-949-016-12456	Sequence 12456, A	376	200.2	22.1	601	4	US-09-949-016-200753	Sequence 200753, A
C 304	201.2	22.2	79835	4	US-09-949-016-16121	Sequence 16121, A	377	200.2	22.1	601	4	US-09-949-016-200754	Sequence 200759, A
C 305	201.2	22.2	79835	4	US-09-949-016-13032	Sequence 13032, A	378	200.2	22.1	601	4	US-09-949-016-200899	Sequence 200899, A
C 306	201.2	22.2	165651	4	US-09-949-016-12882	Sequence 12882, A	379	200.2	22.1	601	4	US-09-949-016-200899	Sequence 200900, A
C 307	201.2	22.2	256176	4	US-09-949-016-15524	Sequence 15524, A	380	200.2	22.1	601	4	US-09-949-016-200900	Sequence 800, Appl
C 308	201.2	22.2	256176	4	US-09-949-016-127563	Sequence 127563, A	381	200.2	22.1	601	4	US-09-949-016-1800	Sequence 13377, A
C 309	201.2	22.2	601	4	US-09-949-016-169369	Sequence 169369, A	382	200.2	22.1	22334	4	US-09-949-016-14948	Sequence 14948, A
C 310	201.2	22.2	601	4	US-09-949-016-170444	Sequence 170444, A	383	200.2	22.1	41663	4	US-09-949-016-12468	Sequence 15882, A
C 311	201.2	22.2	601	4	US-09-949-016-178914	Sequence 178914, A	384	200.2	22.1	44430	4	US-09-949-016-15882	Sequence 13453, A
C 312	201.2	22.2	8180	4	US-09-949-016-14442	Sequence 14442, A	385	200.2	22.1	44431	4	US-09-949-016-13453	Sequence 13454, A
C 313	201.2	22.2	9779	4	US-09-949-016-15370	Sequence 15370, A	386	200.2	22.1	46816	4	US-09-949-016-13018	Sequence 13018, A
C 314	201.2	22.2	14160	4	US-09-949-016-16894	Sequence 16894, A	387	200.2	22.1	46816	4	US-09-949-016-13018	Sequence 14839, A
C 315	201.2	22.2	34011	4	US-09-949-016-12485	Sequence 12485, A	388	200.2	22.1	52636	4	US-09-949-016-14839	Sequence 14831, A
C 316	201.2	22.2	44096	4	US-09-949-016-15208	Sequence 15208, A	389	200.2	22.1	52636	4	US-09-949-016-14839	Sequence 14831, A
C 317	201.2	22.2	81585	4	US-09-949-016-16630	Sequence 16630, A	390	200.2	22.1	52636	4	US-09-949-016-14839	Sequence 14831, A
C 318	201.2	22.2	98828	4	US-09-949-016-16630	Sequence 16630, A	391	200.2	22.1	52636	4	US-09-949-016-14839	Sequence 14831, A
C 319	201.2	22.2	108440	4	US-09-949-016-12085	Sequence 12085, A	392	200.2	22.1	64137	4	US-09-949-016-14831	Sequence 14831, A

C 393	200	22.1	64171	4	US-09-949-016-12502	Sequence 12502, A	C 466	199	21.9	74914	4	US-09-949-016-12286	Sequence 12286, A
C 394	200	22.1	73395	4	US-09-949-016-15151	Sequence 15151, A	C 467	199	21.9	78491	4	US-09-949-016-15132	Sequence 15132, A
C 395	200	22.1	145320	4	US-09-949-016-15858	Sequence 15858, A	C 468	199	21.9	82125	4	US-09-949-016-15317	Sequence 15317, A
C 396	200	22.1	192700	4	US-09-949-016-11820	Sequence 11820, A	C 469	199	21.9	82125	4	US-09-949-016-13518	Sequence 13518, A
C 397	200	22.1	192704	4	US-09-949-016-117182	Sequence 117182, A	C 470	199	21.9	91831	4	US-09-949-016-15095	Sequence 15095, A
C 398	200	22.1	283538	4	US-09-949-016-13506	Sequence 13506, A	C 471	199	21.9	93510	4	US-09-949-016-13694	Sequence 13694, A
C 399	200	22.1	678533	4	US-09-949-016-14577	Sequence 14577, A	C 472	199	21.9	110266	4	US-09-949-016-14913	Sequence 14913, A
C 400	200	22.1	678533	4	US-09-949-016-14578	Sequence 14578, A	C 473	199	21.9	110266	4	US-09-949-016-14914	Sequence 14914, A
C 401	199.8	22.0	601	4	US-09-949-016-3968	Sequence 3968, A	C 474	199	21.9	110266	4	US-09-949-016-14915	Sequence 14915, A
C 402	199.8	22.0	601	4	US-09-949-016-41315	Sequence 41315, A	C 475	199	21.9	110266	4	US-09-949-016-14916	Sequence 14916, A
C 403	199.8	22.0	601	4	US-09-949-016-43318	Sequence 43318, A	C 476	199	21.9	110266	4	US-09-949-016-14917	Sequence 14917, A
C 404	199.8	22.0	601	4	US-09-949-016-43319	Sequence 43319, A	C 477	199	21.9	110266	4	US-09-949-016-14918	Sequence 14918, A
C 405	199.8	22.0	601	4	US-09-949-016-43547	Sequence 43547, A	C 478	199	21.9	110266	4	US-09-949-016-14919	Sequence 14919, A
C 406	199.8	22.0	601	4	US-09-949-016-43548	Sequence 43548, A	C 479	199	21.9	110266	4	US-09-949-016-14920	Sequence 14920, A
C 407	199.8	22.0	601	4	US-09-949-016-43776	Sequence 43776, A	C 480	199	21.9	110266	4	US-09-949-016-14921	Sequence 14921, A
C 408	199.8	22.0	601	4	US-09-949-016-43777	Sequence 43777, A	C 481	199	21.9	110266	4	US-09-949-016-14922	Sequence 14922, A
C 409	199.8	22.0	601	4	US-09-949-016-47534	Sequence 47534, A	C 482	199	21.9	145928	4	US-09-949-016-16476	Sequence 16476, A
C 410	199.8	22.0	601	4	US-09-949-016-82428	Sequence 82428, A	C 483	199	21.9	145928	4	US-09-949-016-15444	Sequence 15444, A
C 411	199.8	22.0	601	4	US-09-949-016-187598	Sequence 187598, A	C 484	199	21.9	145928	4	US-09-801-876B-3	Sequence 3, Appl1
C 412	199.8	22.0	40546	4	US-09-949-016-12847	Sequence 12847, A	C 485	199	21.9	145928	4	US-10-254-869-3	Sequence 3, Appl1
C 413	199.8	22.0	40546	4	US-09-949-016-12915	Sequence 12915, A	C 486	199	21.9	145928	4	US-10-667-442-3	Sequence 3, Appl1
C 414	199.8	22.0	41578	4	US-09-949-016-15245	Sequence 15245, A	C 487	199	21.9	304533	4	US-09-949-016-15371	Sequence 15371, A
C 415	199.8	22.0	75480	4	US-09-949-016-15090	Sequence 15090, A	C 488	199	21.9	304533	4	US-09-949-016-15372	Sequence 15372, A
C 416	199.8	22.0	78720	4	US-09-949-016-12710	Sequence 12710, A	C 489	198.8	21.9	601	4	US-09-949-016-18742	Sequence 18742, A
C 417	199.8	22.0	78720	4	US-09-949-016-17283	Sequence 17283, A	C 490	198.8	21.9	601	4	US-09-949-016-17567	Sequence 17567, A
C 418	199.8	22.0	106924	4	US-09-949-016-13834	Sequence 13834, A	C 491	198.8	21.9	601	4	US-09-949-016-176954	Sequence 176954, A
C 419	199.6	22.0	601	4	US-09-949-016-32182	Sequence 32182, A	C 492	198.8	21.9	7152	3	US-09-167-681-29	Sequence 29, Appl1
C 420	199.6	22.0	601	4	US-09-949-016-60819	Sequence 60819, A	C 493	198.8	21.9	20182	4	US-09-949-016-13240	Sequence 13240, A
C 421	199.6	22.0	601	4	US-09-949-016-112131	Sequence 112131, A	C 494	198.8	21.9	39552	4	US-09-949-016-11799	Sequence 11799, A
C 422	199.6	22.0	601	4	US-09-949-016-146504	Sequence 146504, A	C 495	198.8	21.9	43950	3	US-09-735-934A-3	Sequence 3, Appl1
C 423	199.6	22.0	601	4	US-09-949-016-147535	Sequence 147535, A	C 496	198.8	21.9	43950	4	US-10-060-332-3	Sequence 3, Appl1
C 424	199.6	22.0	26314	4	US-09-949-016-16589	Sequence 16589, A	C 497	198.8	21.9	43950	4	US-10-339-657-3	Sequence 3, Appl1
C 425	199.6	22.0	32278	4	US-09-949-016-14575	Sequence 14575, A	C 498	198.8	21.9	44019	4	US-09-949-016-14902	Sequence 14902, A
C 426	199.6	22.0	36346	4	US-09-949-016-17543	Sequence 17543, A	C 499	198.8	21.9	54779	4	US-09-949-001-27	Sequence 27, Appl1
C 427	199.6	22.0	51062	4	US-09-949-016-14725	Sequence 14725, A	C 500	198.8	21.9	54780	4	US-09-949-001-39	Sequence 39, Appl1
C 428	199.6	22.0	105189	4	US-09-949-016-13029	Sequence 13029, A	C 501	198.8	21.9	55114	4	US-09-949-016-16792	Sequence 16792, A
C 429	199.4	22.0	601	4	US-09-949-016-64118	Sequence 64118, A	C 502	198.8	21.9	87039	4	US-09-949-016-15691	Sequence 15691, A
C 430	199.4	22.0	601	4	US-09-949-016-70685	Sequence 70685, A	C 503	198.8	21.9	113379	4	US-09-949-016-17561	Sequence 17561, A
C 431	199.4	22.0	601	4	US-09-949-016-70686	Sequence 70686, A	C 504	198.8	21.9	113379	4	US-09-949-016-17562	Sequence 17562, A
C 432	199.4	22.0	23826	4	US-09-949-016-16712	Sequence 16712, A	C 505	198.8	21.9	124480	4	US-09-949-016-15921	Sequence 15921, A
C 433	199.4	22.0	23826	4	US-09-949-016-16713	Sequence 16713, A	C 506	198.8	21.9	223471	4	US-09-949-016-12387	Sequence 12387, A
C 434	199.4	22.0	23826	4	US-09-949-016-16714	Sequence 16714, A	C 507	198.8	21.9	223471	4	US-09-949-016-12784	Sequence 12784, A
C 435	199.4	22.0	23826	4	US-09-949-016-16715	Sequence 16715, A	C 508	198.8	21.9	223471	4	US-09-949-016-12725	Sequence 12725, A
C 436	199.4	22.0	43192	4	US-09-949-016-15665	Sequence 15665, A	C 509	198.8	21.9	276687	4	US-09-949-016-13840	Sequence 13840, A
C 437	199.4	22.0	93971	4	US-09-949-016-16097	Sequence 16097, A	C 510	198.6	21.9	601	4	US-09-949-016-76001	Sequence 76001, A
C 438	199.4	22.0	93971	4	US-09-949-016-16098	Sequence 16098, A	C 511	198.6	21.9	601	4	US-09-949-016-127637	Sequence 127637, A
C 439	199.4	22.0	145928	4	US-09-949-016-15444	Sequence 15444, A	C 512	198.6	21.9	601	4	US-09-949-016-127974	Sequence 127974, A
C 440	199.4	22.0	176006	4	US-09-949-016-16804	Sequence 16804, A	C 513	198.6	21.9	601	4	US-09-949-016-131654	Sequence 131654, A
C 441	199.4	22.0	253375	4	US-09-949-016-12849	Sequence 12849, A	C 514	198.6	21.9	1946	4	US-09-620-312D-462	Sequence 462, App
C 442	199.2	22.0	601	4	US-09-949-016-69950	Sequence 69950, A	C 515	198.6	21.9	15297	3	US-09-817-180-3	Sequence 3, Appl1
C 443	199.2	22.0	29907	4	US-09-949-016-13395	Sequence 13395, A	C 516	198.6	21.9	15297	4	US-10-003-295-3	Sequence 3, Appl1
C 444	199.2	22.0	29913	4	US-09-949-016-14811	Sequence 12481, A	C 517	198.6	21.9	45183	4	US-09-949-016-12798	Sequence 12798, A
C 445	199.2	22.0	31820	4	US-09-949-016-13356	Sequence 13356, A	C 518	198.6	21.9	52789	4	US-09-949-016-12130	Sequence 12130, A
C 446	199.2	22.0	37215	4	US-09-949-016-15526	Sequence 15526, A	C 519	198.6	21.9	95790	4	US-09-949-016-16641	Sequence 16641, A
C 447	199.2	22.0	91279	4	US-09-949-016-15146	Sequence 15146, A	C 520	198.6	21.9	95240	4	US-09-949-016-11933	Sequence 11933, A
C 448	199.2	22.0	100463	4	US-09-949-016-12511	Sequence 12511, A	C 521	198.6	21.9	60137	4	US-09-949-016-14735	Sequence 14735, A
C 449	199.2	22.0	100468	4	US-09-949-016-13725	Sequence 13725, A	C 522	198.6	21.9	60137	4	US-09-949-016-14912	Sequence 14912, A
C 450	199.2	22.0	194537	4	US-09-949-016-13928	Sequence 13928, A	C 523	198.6	21.9	67581	4	US-09-949-016-14768	Sequence 14768, A
C 451	199.2	22.0	201529	4	US-09-949-016-12740	Sequence 12740, A	C 524	198.6	21.9	67643	4	US-09-949-016-14760	Sequence 14760, A
C 452	199.2	22.0	304533	4	US-09-949-016-15371	Sequence 15371, A	C 525	198.6	21.9	86612	4	US-09-949-016-16803	Sequence 16803, A
C 453	199.2	22.0	304533	4	US-09-949-016-15372	Sequence 15372, A	C 526	198.6	21.9	90724	4	US-09-949-016-16601	Sequence 16601, A
C 454	199	21.9	601	4	US-09-949-016-61837	Sequence 61837, A	C 527	198.6	21.9	96922	4	US-09-949-016-17061	Sequence 17061, A
C 455	199	21.9	8374	4	US-09-949-016-15257	Sequence 15257, A	C 528	198.6	21.9	97195	4	US-09-949-016-12212	Sequence 12212, A
C 456	199	21.9	10546	4	US-09-949-016-15624	Sequence 15624, A	C 529	198.6	21.9	97196	4	US-09-949-016-16971	Sequence 16971, A
C 457	199	21.9	17154	4	US-09-949-016-15889	Sequence 15889, A	C 530	198.6	21.9	96962	4	US-09-949-016-14133	Sequence 14133, A
C 458	199	21.9	19503	4	US-09-949-016-16528	Sequence 16528, A	C 531	198.6	21.9	102053	4	US-09-949-016-13025	Sequence 13025, A
C 459	199	21.9	24205	4	US-09-949-016-15385	Sequence 15385, A	C 532	198.6	21.9	102884	4	US-09-949-016-17100	Sequence 17100, A
C 460	199	21.9	39982	4	US-09-820-924-3	Sequence 3, Appl1	C 533	198.6	21.9	112883	4	US-09-949-016-16976	Sequence 16976, A
C 461	199	21.9	39982	4	US-10-369-626-3	Sequence 3, Appl1	C 534	198.6	21.9	112883	4	US-09-949-016-16977	Sequence 16977, A
C 462	199	21.9	40493	4	US-09-949-016-15453	Sequence 15453, A	C 535	198.6	21.9	11649	4	US-09-949-016-12537	Sequence 12537, A
C 463	199	21.9	51046	4	US-09-949-016-12739	Sequence 12739, A	C 536	198.6	21.9	157866	4	US-09-949-016-12982	Sequence 12982, A
C 464	199	21.9	51046	4	US-09-949-016-13946	Sequence 13946, A	C 537	198.6	21.9	157866	4	US-09-949-016-12983	Sequence 12983, A
C 465	199	21.9	74881	4	US-09-949-016-15545	Sequence 15545, A	C 538	198.6	21.9	157866	4	US-09-949-016-12984	Sequence 12984, A

C 539	198.4	21.9	601	4	US-09-949-016-150106	Sequence 150106,	C 612	198	21.8	601	4	US-09-949-016-44634	Sequence 44634, A
540	198.4	21.9	601	4	US-09-949-016-156839	Sequence 156839,	613	198	21.8	601	4	US-09-949-016-88078	Sequence 88078, A
541	198.4	21.9	601	4	US-09-949-016-171105	Sequence 171105,	614	198	21.8	601	4	US-09-949-016-136816	Sequence 136816,
542	198.4	21.9	601	4	US-09-949-016-171235	Sequence 171235,	615	198	21.8	601	4	US-09-949-016-140334	Sequence 140334,
543	198.4	21.9	7705	2	US-08-687-080-115	Sequence 115, App	616	198	21.8	601	4	US-09-949-016-150107	Sequence 150107,
544	198.4	21.9	15586	4	US-09-949-016-13899	Sequence 13899, A	617	198	21.8	601	4	US-09-949-016-160816	Sequence 160816,
545	198.4	21.9	20441	4	US-09-949-016-13052	Sequence 13052, A	618	198	21.8	601	4	US-09-949-016-160817	Sequence 160817,
546	198.4	21.9	22010	4	US-09-949-016-15960	Sequence 15960, A	619	198	21.8	601	4	US-09-949-016-164502	Sequence 164502,
C 547	198.4	21.9	40333	4	US-09-949-016-11821	Sequence 11821,	620	198	21.8	601	4	US-09-949-016-164502	Sequence 172475,
C 548	198.4	21.9	40332	4	US-09-949-016-13982	Sequence 13982, A	621	198	21.8	13634	4	US-09-949-016-172475	Sequence 16376, A
549	198.4	21.9	45437	4	US-09-949-016-16343	Sequence 16343, A	622	198	21.8	23301	4	US-09-949-016-16773	Sequence 16773, A
C 550	198.4	21.9	50797	4	US-09-949-016-16346	Sequence 16346, A	623	198	21.8	33731	4	US-09-949-016-13473	Sequence 13473, A
C 551	198.4	21.9	50797	4	US-09-949-016-16347	Sequence 16347, A	624	198	21.8	33731	4	US-09-949-016-13474	Sequence 13470, A
C 552	198.4	21.9	51273	4	US-09-949-016-13018	Sequence 13018, A	625	198	21.8	38803	4	US-09-949-016-117570	Sequence 13471, A
C 553	198.4	21.9	72278	4	US-09-949-016-16113	Sequence 16113, A	626	198	21.8	38814	4	US-09-949-016-13471	Sequence 13471, A
C 554	198.4	21.9	85854	4	US-09-949-016-12908	Sequence 12908, A	627	198	21.8	39528	4	US-09-949-016-11790	Sequence 11790, A
555	198.4	21.9	107329	4	US-09-949-016-12663	Sequence 12663, A	628	198	21.8	39528	4	US-09-949-016-15475	Sequence 15475, A
556	198.4	21.9	107339	4	US-09-949-016-12664	Sequence 12664, A	629	198	21.8	39529	4	US-09-949-016-12454	Sequence 12454, A
557	198.4	21.9	107330	4	US-09-949-016-15408	Sequence 15408, A	C 630	198	21.8	39715	4	US-09-949-016-14802	Sequence 14902, A
558	198.4	21.9	107330	4	US-09-949-016-15409	Sequence 15409, A	631	198	21.8	44019	4	US-09-949-016-14802	Sequence 16054, A
559	198.4	21.9	107330	4	US-09-949-016-15410	Sequence 15410, A	632	198	21.8	51336	4	US-09-949-016-16054	Sequence 16792, A
560	198.4	21.9	107330	4	US-09-949-016-15411	Sequence 15411, A	633	198	21.8	55114	4	US-09-949-016-16792	Sequence 16819, A
561	198.4	21.9	107750	4	US-09-949-016-12662	Sequence 12662, A	634	198	21.8	70000	3	US-09-851-896-3	Sequence 3, Appl1
562	198.4	21.9	107751	4	US-09-949-016-13412	Sequence 13412, A	635	198	21.8	76399	4	US-09-949-016-16819	Sequence 16819, A
563	198.4	21.9	107751	4	US-09-949-016-15413	Sequence 15413, A	C 636	198	21.8	85863	4	US-09-949-016-16819	Sequence 16151, A
564	198.4	21.9	107751	4	US-09-949-016-15414	Sequence 15414, A	C 637	197.8	21.8	146801	4	US-09-949-016-16151	Sequence 61838, A
565	198.4	21.9	107751	4	US-09-949-016-15415	Sequence 15415, A	638	197.8	21.8	601	4	US-09-949-016-64117	Sequence 64117, A
566	198.4	21.9	107925	4	US-09-949-016-11875	Sequence 11875, A	C 639	197.8	21.8	601	4	US-09-949-016-109524	Sequence 109524, A
567	198.4	21.9	107926	4	US-09-949-016-15405	Sequence 15405, A	C 640	197.8	21.8	601	4	US-09-949-016-109524	Sequence 109777, A
568	198.4	21.9	107926	4	US-09-949-016-15405	Sequence 15405, A	C 641	197.8	21.8	601	4	US-09-949-016-109777	Sequence 131748, A
569	198.4	21.9	107926	4	US-09-949-016-15406	Sequence 15406, A	642	197.8	21.8	601	4	US-09-949-016-131748	Sequence 148576, A
570	198.4	21.9	107926	4	US-09-949-016-15407	Sequence 15407, A	643	197.8	21.8	601	4	US-09-949-016-148576	Sequence 148592, A
C 571	198.4	21.9	133384	4	US-09-949-016-16964	Sequence 16964, A	644	197.8	21.8	601	4	US-09-949-016-148592	Sequence 176106, A
C 572	198.4	21.9	133384	4	US-09-949-016-16964	Sequence 16964, A	645	197.8	21.8	601	4	US-09-949-016-176106	Sequence 9, Appl1
C 573	198.4	21.9	143971	4	US-09-949-016-12651	Sequence 12651, A	646	197.8	21.8	3129	4	US-10-045-428A-9	Sequence 15798, A
C 574	198.4	21.9	191433	4	US-09-949-016-16144	Sequence 16144, A	647	197.8	21.8	8412	4	US-09-949-016-16798	Sequence 16798, A
C 575	198.4	21.9	268449	4	US-09-949-016-17244	Sequence 17244, A	648	197.8	21.8	12797	4	US-09-949-016-16798	Sequence 16798, A
576	198.4	21.9	601	4	US-09-949-016-33302	Sequence 33302, A	C 649	197.8	21.8	15778	4	US-09-949-016-113538	Sequence 13510, A
577	198.2	21.9	601	4	US-09-949-016-33303	Sequence 33303, A	C 650	197.8	21.8	18620	4	US-09-949-016-113510	Sequence 11851, A
578	198.2	21.9	601	4	US-09-949-016-33304	Sequence 33304, A	651	197.8	21.8	24523	4	US-09-949-016-11853	Sequence 15707, A
C 579	198.2	21.9	601	4	US-09-949-016-38607	Sequence 38607, A	652	197.8	21.8	25202	4	US-09-949-016-13151	Sequence 13151, A
580	198.2	21.9	601	4	US-09-949-016-82427	Sequence 82427, A	653	197.8	21.8	53526	3	US-08-658-136-2	Sequence 2, Appl1
581	198.2	21.9	601	4	US-09-949-016-137405	Sequence 137405, A	654	197.8	21.8	53577	3	US-08-658-136-1	Sequence 1, Appl1
582	198.2	21.9	601	4	US-09-949-016-167373	Sequence 167373, A	655	197.8	21.8	56904	4	US-09-949-016-15501	Sequence 15501, A
583	198.2	21.9	601	4	US-09-949-016-176953	Sequence 176953, A	656	197.8	21.8	80411	4	US-09-949-016-15777	Sequence 15777, A
C 584	198.2	21.9	601	4	US-09-949-016-186050	Sequence 186050, A	657	197.8	21.8	92304	4	US-09-949-016-15943	Sequence 15943, A
585	198.2	21.9	601	4	US-09-949-016-187597	Sequence 187597, A	658	197.8	21.8	98302	4	US-09-949-016-16847	Sequence 16847, A
C 586	198.2	21.9	14345	4	US-09-949-016-15449	Sequence 15449, A	659	197.8	21.8	112507	4	US-09-949-016-16847	Sequence 16847, A
587	198.2	21.9	21535	4	US-09-949-016-12826	Sequence 12826, A	C 660	197.8	21.8	112507	4	US-09-949-016-12794	Sequence 12794, A
588	198.2	21.9	21535	4	US-09-949-016-12827	Sequence 12827, A	C 661	197.8	21.8	112507	4	US-09-949-016-12794	Sequence 12794, A
589	198.2	21.9	21535	4	US-09-949-016-12828	Sequence 12828, A	C 662	197.8	21.8	112508	4	US-09-949-016-16589	Sequence 16589, A
590	198.2	21.9	21535	4	US-09-949-016-12829	Sequence 12829, A	C 663	197.8	21.8	112508	4	US-09-949-016-16590	Sequence 16590, A
591	198.2	21.9	21536	4	US-09-949-016-13366	Sequence 13366, A	C 664	197.8	21.8	137949	4	US-09-949-016-12196	Sequence 12196, A
592	198.2	21.9	21536	4	US-09-949-016-13367	Sequence 13367, A	C 665	197.8	21.8	137956	4	US-09-949-016-12196	Sequence 12196, A
593	198.2	21.9	21536	4	US-09-949-016-13368	Sequence 13368, A	C 666	197.8	21.8	143155	4	US-09-949-016-11925	Sequence 11925, A
594	198.2	21.9	21536	4	US-09-949-016-13369	Sequence 13369, A	C 667	197.8	21.8	143156	4	US-09-949-016-14368	Sequence 14368, A
595	198.2	21.9	22634	4	US-09-949-016-16666	Sequence 16666, A	C 668	197.8	21.8	143156	4	US-09-949-016-14368	Sequence 14368, A
596	198.2	21.9	36180	4	US-09-949-016-11745	Sequence 11745, A	C 669	197.8	21.8	157832	4	US-09-949-016-16723	Sequence 16723, A
597	198.2	21.9	36181	4	US-09-949-016-16133	Sequence 16133, A	C 670	197.8	21.8	162480	3	US-09-345-882-1	Sequence 1, Appl1
C 598	198.2	21.9	36228	4	US-09-949-016-12256	Sequence 12256, A	671	197.8	21.8	189560	4	US-09-949-016-11702	Sequence 17020, A
C 599	198.2	21.9	36228	4	US-09-949-016-15468	Sequence 15468, A	672	197.8	21.8	198942	4	US-09-949-016-11702	Sequence 13209, A
600	198.2	21.9	39243	4	US-09-949-016-12316	Sequence 12316, A	673	197.8	21.8	246444	4	US-09-949-016-13113	Sequence 13113, A
601	198.2	21.9	39243	4	US-09-949-016-15443	Sequence 15443, A	674	197.8	21.8	325791	4	US-09-949-016-13113	Sequence 1, Appl1
602	198.2	21.9	44988	4	US-09-949-016-16344	Sequence 16344, A	675	197.6	21.8	601	4	US-09-168-185A-1	Sequence 69951, A
603	198.2	21.9	47887	4	US-09-949-016-11959	Sequence 11959, A	C 676	197.6	21.8	601	4	US-09-949-016-115572	Sequence 115572, A
C 604	198.2	21.9	84870	4	US-09-949-016-17347	Sequence 17347, A	C 677	197.6	21.8	601	4	US-09-949-016-115655	Sequence 115655, A
C 605	198.2	21.9	96074	4	US-09-949-016-12760	Sequence 12760, A	C 678	197.6	21.8	601	4	US-09-949-016-115758	Sequence 115758, A
C 606	198.2	21.9	96074	4	US-09-949-016-12760	Sequence 12760, A	C 679	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
C 607	198.2	21.9	96074	4	US-09-949-016-13611	Sequence 13611, A	C 680	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
C 608	198.2	21.9	96074	4	US-09-949-016-13611	Sequence 13611, A	C 681	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
609	198.2	21.9	123202	4	US-09-949-016-15270	Sequence 15270, A	C 682	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
610	198	21.8	601	4	US-09-949-016-33412	Sequence 33412, A	C 683	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
611	198	21.8	601	4	US-09-949-016-41047	Sequence 41047, A	C 684	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A

C 685	197.6	21.8	601	4	US-09-949-016-116409	Sequence 116409,	758	197.2	21.7	41125	4	US-09-949-016-12413	Sequence 12413, A
C 686	197.6	21.8	601	4	US-09-949-016-176518	Sequence 176518,	759	197.2	21.7	41126	4	US-09-949-016-11273	Sequence 17273, A
C 687	197.6	21.8	26611	4	US-09-949-016-164884	Sequence 16484, A	760	197.2	21.7	61461	4	US-09-949-016-15419	Sequence 15419, A
C 688	197.6	21.8	38808	4	US-09-949-016-11802	Sequence 11802, A	761	197.2	21.7	62908	4	US-09-949-016-17554	Sequence 17554, A
C 689	197.6	21.8	38808	4	US-09-949-016-16735	Sequence 16735, A	762	197.2	21.7	76610	4	US-09-949-016-15521	Sequence 15521, A
C 690	197.6	21.8	46433	4	US-09-949-016-16824	Sequence 16824, A	763	197.2	21.7	83697	4	US-09-949-016-16040	Sequence 16040, A
C 691	197.6	21.8	53108	4	US-09-949-016-16681	Sequence 16681, A	764	197.2	21.7	85854	4	US-09-949-016-12908	Sequence 12908, A
C 692	197.6	21.8	59139	4	US-09-949-016-16115	Sequence 16115, A	765	197.2	21.7	92139	4	US-09-918-686-1	Sequence 1, Appl1
C 693	197.6	21.8	66164	4	US-09-949-016-17574	Sequence 13574, A	766	197.2	21.7	197875	4	US-09-949-016-15425	Sequence 15425, A
C 694	197.6	21.8	119762	4	US-09-949-016-17133	Sequence 17133, A	767	197.2	21.7	248968	4	US-09-949-016-12614	Sequence 12614, A
C 695	197.6	21.8	119981	4	US-09-949-016-11844	Sequence 11844, A	768	197	21.7	601	4	US-09-949-016-78179	Sequence 78179, A
C 696	197.6	21.8	119982	4	US-09-949-016-13606	Sequence 13606, A	769	197	21.7	601	4	US-09-949-016-113846	Sequence 113846, A
C 697	197.6	21.8	139150	4	US-09-949-016-17398	Sequence 17398, A	770	197	21.7	601	4	US-09-949-016-114014	Sequence 114014, A
C 698	197.6	21.8	139577	4	US-09-949-016-12879	Sequence 12879, A	771	197	21.7	601	4	US-09-949-016-114182	Sequence 114182, A
C 699	197.6	21.8	194915	4	US-09-949-016-15884	Sequence 15584, A	772	197	21.7	601	4	US-09-949-016-114330	Sequence 114330, A
C 700	197.6	21.8	300402	4	US-09-949-016-13632	Sequence 13632, A	773	197	21.7	601	4	US-09-949-016-114518	Sequence 114518, A
C 701	197.4	21.8	601	4	US-09-949-016-21510	Sequence 21510, A	774	197	21.7	601	4	US-09-949-016-114686	Sequence 114686, A
C 702	197.4	21.8	601	4	US-09-949-016-36770	Sequence 36770, A	775	197	21.7	601	4	US-09-949-016-114854	Sequence 114854, A
C 703	197.4	21.8	601	4	US-09-949-016-91427	Sequence 91427, A	776	197	21.7	601	4	US-09-949-016-114854	Sequence 114854, A
C 704	197.4	21.8	601	4	US-09-949-016-91427	Sequence 91427, A	777	197	21.7	8396	3	US-09-328-174A-1	Sequence 1, Appl1
C 705	197.4	21.8	601	4	US-09-949-016-122955	Sequence 122955, A	778	197	21.7	8409	3	US-09-167-681-37	Sequence 37, Appl1
C 706	197.4	21.8	601	4	US-09-949-016-123049	Sequence 123049, A	779	197	21.7	15615	4	US-09-949-016-17221	Sequence 17221, A
C 707	197.4	21.8	601	4	US-09-949-016-123143	Sequence 123143, A	780	197	21.7	18319	4	US-09-949-016-17446	Sequence 17446, A
C 708	197.4	21.8	601	4	US-09-949-016-123237	Sequence 123237, A	781	197	21.7	20610	4	US-09-949-016-146104	Sequence 146104, A
C 709	197.4	21.8	601	4	US-09-949-016-123331	Sequence 123331, A	782	197	21.7	33327	4	US-09-949-016-14108	Sequence 14108, A
C 710	197.4	21.8	601	4	US-09-949-016-123373	Sequence 123373, A	783	197	21.7	34548	4	US-09-949-016-12681	Sequence 12681, A
C 711	197.4	21.8	601	4	US-09-949-016-123415	Sequence 123415, A	784	197	21.7	34548	4	US-09-949-016-16124	Sequence 16124, A
C 712	197.4	21.8	601	4	US-09-949-016-123457	Sequence 123457, A	785	197	21.7	39032	4	US-09-949-016-12874	Sequence 12874, A
C 713	197.4	21.8	601	4	US-09-949-016-123499	Sequence 123499, A	786	197	21.7	39039	4	US-09-949-016-16462	Sequence 16462, A
C 714	197.4	21.8	601	4	US-09-949-016-123541	Sequence 123541, A	787	197	21.7	41639	4	US-09-949-016-15471	Sequence 15471, A
C 715	197.4	21.8	601	4	US-09-949-016-123583	Sequence 123583, A	788	197	21.7	44608	4	US-09-949-016-15604	Sequence 15604, A
C 716	197.4	21.8	601	4	US-09-949-016-123625	Sequence 123625, A	789	197	21.7	44971	4	US-09-949-016-17049	Sequence 17049, A
C 717	197.4	21.8	601	4	US-09-949-016-123667	Sequence 123667, A	790	197	21.7	55665	4	US-09-949-016-14026	Sequence 14026, A
C 718	197.4	21.8	601	4	US-09-949-016-123709	Sequence 123709, A	791	197	21.7	60424	4	US-09-949-016-12175	Sequence 12175, A
C 719	197.4	21.8	601	4	US-09-949-016-123751	Sequence 123751, A	792	197	21.7	65300	4	US-09-949-016-16813	Sequence 16813, A
C 720	197.4	21.8	601	4	US-09-949-016-138053	Sequence 138053, A	793	197	21.7	66428	4	US-09-949-016-12917	Sequence 12917, A
C 721	197.4	21.8	601	4	US-09-949-016-154829	Sequence 154829, A	794	197	21.7	77535	4	US-09-949-016-14280	Sequence 14280, A
C 722	197.4	21.8	601	4	US-09-949-016-171104	Sequence 171104, A	795	197	21.7	77535	4	US-09-949-016-14281	Sequence 14281, A
C 723	197.4	21.8	601	4	US-09-949-016-171234	Sequence 171234, A	796	197	21.7	107421	4	US-09-949-016-15532	Sequence 15532, A
C 724	197.4	21.8	601	4	US-09-949-016-158058	Sequence 158058, A	797	197	21.7	121982	4	US-09-949-016-12085	Sequence 12085, A
C 725	197.4	21.8	15148	4	US-09-949-016-15958	Sequence 15958, A	798	197	21.7	121982	4	US-09-949-016-14105	Sequence 14105, A
C 726	197.4	21.8	27555	4	US-09-949-016-17466	Sequence 17466, A	799	197	21.7	121982	4	US-09-949-016-15092	Sequence 15092, A
C 727	197.4	21.8	31469	4	US-09-949-016-13722	Sequence 13722, A	800	197	21.7	133719	4	US-09-949-016-12095	Sequence 12095, A
C 728	197.4	21.8	34330	4	US-09-949-016-12052	Sequence 12052, A	801	196.8	21.7	601	4	US-09-949-016-109491	Sequence 80709, A
C 729	197.4	21.8	38954	4	US-09-949-016-112922	Sequence 12422, A	802	196.8	21.7	601	4	US-09-949-016-168079	Sequence 168079, A
C 730	197.4	21.8	79350	4	US-09-949-016-12467	Sequence 12467, A	803	196.8	21.7	601	4	US-09-949-016-162049	Sequence 162049, A
C 731	197.4	21.8	79351	4	US-09-949-016-16275	Sequence 16275, A	804	196.8	21.7	601	4	US-09-949-016-162049	Sequence 162049, A
C 732	197.4	21.8	84875	4	US-09-949-016-17334	Sequence 17334, A	805	196.8	21.7	13948	4	US-09-949-016-165965	Sequence 165965, A
C 733	197.4	21.8	84875	4	US-09-949-016-17335	Sequence 17335, A	806	196.8	21.7	13948	4	US-09-949-016-13023	Sequence 13023, A
C 734	197.4	21.8	84875	4	US-09-949-016-17336	Sequence 17336, A	807	196.8	21.7	13948	4	US-09-949-016-13061	Sequence 13061, A
C 735	197.4	21.8	84875	4	US-09-949-016-17337	Sequence 17337, A	808	196.8	21.7	27659	4	US-09-949-016-17612	Sequence 17612, A
C 736	197.4	21.8	85152	4	US-09-949-016-12665	Sequence 12665, A	809	196.8	21.7	28321	4	US-09-949-016-11936	Sequence 11936, A
C 737	197.4	21.8	85152	4	US-09-949-016-12666	Sequence 12666, A	810	196.8	21.7	28325	4	US-09-949-016-16622	Sequence 16622, A
C 738	197.4	21.8	85152	4	US-09-949-016-12667	Sequence 12667, A	811	196.8	21.7	35417	4	US-09-949-016-16129	Sequence 16129, A
C 739	197.4	21.8	85152	4	US-09-949-016-12668	Sequence 12668, A	812	196.8	21.7	41617	4	US-09-949-016-14356	Sequence 14356, A
C 740	197.4	21.8	96645	4	US-09-949-016-13658	Sequence 13658, A	813	196.8	21.7	41618	4	US-09-949-016-14361	Sequence 14361, A
C 741	197.4	21.8	128470	4	US-09-949-016-13765	Sequence 13765, A	814	196.8	21.7	44052	4	US-09-949-016-16341	Sequence 16341, A
C 742	197.4	21.8	128470	4	US-09-949-016-15127	Sequence 15127, A	815	196.8	21.7	44052	4	US-09-949-016-12203	Sequence 12203, A
C 743	197.4	21.8	192506	4	US-09-949-016-15830	Sequence 15830, A	816	196.8	21.7	54878	4	US-09-949-016-12255	Sequence 12255, A
C 744	197.4	21.8	300402	4	US-09-949-016-13632	Sequence 13632, A	817	196.8	21.7	70000	3	US-09-949-016-15580	Sequence 3, Appl1
C 745	197.4	21.8	300402	4	US-09-949-016-11868	Sequence 11868, A	818	196.8	21.7	70000	3	US-09-949-016-15580	Sequence 15580, A
C 746	197.4	21.8	302604	4	US-09-949-016-14589	Sequence 14589, A	819	196.8	21.7	72592	4	US-09-949-016-17592	Sequence 17592, A
C 747	197.4	21.8	302604	4	US-09-949-016-14589	Sequence 14589, A	820	196.8	21.7	72592	4	US-09-949-016-16819	Sequence 16819, A
C 748	197.4	21.8	308362	4	US-09-949-016-17119	Sequence 17119, A	821	196.8	21.7	78846	4	US-09-949-016-12396	Sequence 12396, A
C 749	197.2	21.7	282	1	US-08-133-623-8	Sequence 8, Appl1	822	196.8	21.7	78846	4	US-09-949-016-12791	Sequence 12791, A
C 750	197.2	21.7	449	4	US-09-621-976-16908	Sequence 16908, A	823	196.8	21.7	78846	4	US-09-949-016-12792	Sequence 12792, A
C 751	197.2	21.7	601	4	US-09-949-016-184729	Sequence 184729, A	824	196.8	21.7	78846	4	US-09-949-016-12793	Sequence 12793, A
C 752	197.2	21.7	7644	4	US-09-953-318-20	Sequence 20, Appl1	825	196.8	21.7	78850	4	US-09-949-016-16013	Sequence 16013, A
C 753	197.2	21.7	7644	4	US-09-949-016-17610	Sequence 17610, A	826	196.8	21.7	78850	4	US-09-949-016-16014	Sequence 16014, A
C 754	197.2	21.7	31232	4	US-09-949-016-12619	Sequence 12619, A	827	196.8	21.7	78850	4	US-09-949-016-16015	Sequence 16015, A
C 755	197.2	21.7	31231	4	US-09-949-016-15766	Sequence 15766, A	828	196.8	21.7	78850	4	US-09-949-016-16016	Sequence 16016, A
C 756	197.2	21.7	40936	4	US-09-949-016-16607	Sequence 16607, A	829	196.8	21.7	78850	4	US-09-949-016-16201	Sequence 16201, A
C 757	197.2	21.7	40936	4	US-09-949-016-16608	Sequence 16608, A	830	196.8	21.7	78850	4	US-09-949-016-16202	Sequence 16202, A

C 831	196.8	21.7	78850	4	US-09-949-016-16203	Sequence 16203, A	904	196.4	21.7	601	4	US-09-949-016-171106	Sequence 171106, A
C 832	196.8	21.7	78850	4	US-09-949-016-16204	Sequence 16204, A	905	196.4	21.7	601	4	US-09-949-016-171235	Sequence 171235, A
C 833	196.8	21.7	79350	4	US-09-949-016-12467	Sequence 12467, A	906	196.4	21.7	601	4	US-09-949-016-175176	Sequence 175176, A
C 834	196.8	21.7	79351	4	US-09-949-016-16275	Sequence 16275, A	C 907	196.4	21.7	601	4	US-09-949-016-175187	Sequence 175187, A
C 835	196.8	21.7	80858	4	US-09-949-016-12659	Sequence 12659, A	C 908	196.4	21.7	601	4	US-09-949-016-175198	Sequence 175198, A
C 836	196.8	21.7	80859	4	US-09-949-016-15715	Sequence 15715, A	C 909	196.4	21.7	601	4	US-09-949-016-175209	Sequence 175209, A
C 837	196.8	21.7	90472	4	US-09-949-016-14038	Sequence 14038, A	C 910	196.4	21.7	14185	4	US-09-949-016-14809	Sequence 14809, A
C 838	196.8	21.7	90473	4	US-09-949-016-12063	Sequence 12063, A	C 911	196.4	21.7	14754	4	US-09-949-016-13636	Sequence 13636, A
C 839	196.8	21.7	95020	4	US-09-949-016-13272	Sequence 13272, A	C 912	196.4	21.7	17085	4	US-09-949-016-16507	Sequence 16507, A
C 840	196.8	21.7	106077	4	US-09-949-016-13593	Sequence 13593, A	C 913	196.4	21.7	20852	4	US-09-949-016-14974	Sequence 14974, A
C 841	196.8	21.7	149543	4	US-09-949-016-15947	Sequence 15947, A	C 914	196.4	21.7	25166	4	US-09-949-016-16072	Sequence 16072, A
C 842	196.8	21.7	260283	4	US-09-949-016-12106	Sequence 12106, A	C 915	196.4	21.7	29686	4	US-09-949-016-16379	Sequence 16379, A
C 843	196.8	21.7	260296	4	US-09-949-016-12505	Sequence 12505, A	C 916	196.4	21.7	30787	4	US-09-949-016-13724	Sequence 13724, A
C 844	196.8	21.7	670689	4	US-09-949-016-14207	Sequence 14207, A	C 917	196.4	21.7	31667	4	US-09-949-016-13134	Sequence 13134, A
C 845	196.8	21.7	670690	4	US-09-949-016-14207	Sequence 14207, A	C 918	196.4	21.7	31868	4	US-09-949-016-11907	Sequence 11907, A
C 846	196.6	21.7	461	3	US-09-404-879A-3	Sequence 1, Appl1	C 919	196.4	21.7	40897	4	US-09-949-016-13911	Sequence 13911, A
C 847	196.6	21.7	461	3	US-09-338-933-1	Sequence 1, Appl1	C 920	196.4	21.7	40897	4	US-09-949-016-13911	Sequence 13911, A
C 848	196.6	21.7	461	3	US-09-338-933-1	Sequence 1, Appl1	C 921	196.4	21.7	40897	4	US-09-949-016-13912	Sequence 13912, A
C 849	196.6	21.7	461	4	US-09-338-933-3	Sequence 3, Appl1	C 922	196.4	21.7	40897	4	US-09-949-016-13912	Sequence 13912, A
C 850	196.6	21.7	461	4	US-09-215-681-1	Sequence 1, Appl1	C 923	196.4	21.7	40897	4	US-09-949-016-14409	Sequence 14409, A
C 851	196.6	21.7	461	4	US-09-215-681-3	Sequence 3, Appl1	C 924	196.4	21.7	40897	4	US-09-949-016-14410	Sequence 14410, A
C 852	196.6	21.7	461	4	US-09-215-681-3	Sequence 3, Appl1	C 925	196.4	21.7	40897	4	US-09-949-016-14411	Sequence 14411, A
C 853	196.6	21.7	461	4	US-09-215-681-3	Sequence 3, Appl1	C 926	196.4	21.7	40897	4	US-09-949-016-14412	Sequence 14412, A
C 854	196.6	21.7	461	4	US-09-215-681-3	Sequence 3, Appl1	C 927	196.4	21.7	40897	4	US-09-949-016-14413	Sequence 14413, A
C 855	196.6	21.7	461	4	US-09-215-681-3	Sequence 3, Appl1	C 928	196.4	21.7	40897	4	US-09-949-016-14414	Sequence 14414, A
C 856	196.6	21.7	461	4	US-09-949-016-163002	Sequence 163002, A	C 929	196.4	21.7	55675	4	US-09-949-016-15706	Sequence 15706, A
C 857	196.6	21.7	601	4	US-09-949-016-167371	Sequence 167371, A	C 930	196.4	21.7	66628	4	US-09-949-016-12630	Sequence 12630, A
C 858	196.6	21.7	601	4	US-09-949-016-167372	Sequence 167372, A	C 931	196.4	21.7	66628	4	US-09-949-016-16112	Sequence 16112, A
C 859	196.6	21.7	601	4	US-09-949-016-169148	Sequence 169148, A	C 932	196.4	21.7	82494	4	US-09-949-016-15096	Sequence 15096, A
C 860	196.6	21.7	601	4	US-09-949-016-16468	Sequence 16468, Ap	C 933	196.4	21.7	93778	4	US-09-949-016-14913	Sequence 14913, A
C 861	196.6	21.7	4014	4	US-09-949-016-6468	Sequence 14649, Ap	C 934	196.4	21.7	110266	4	US-09-949-016-18914	Sequence 14914, A
C 862	196.6	21.7	12394	3	US-09-488-856A-10	Sequence 10, Appl1	C 935	196.4	21.7	110266	4	US-09-949-016-18914	Sequence 14914, A
C 863	196.6	21.7	14781	4	US-09-949-016-15917	Sequence 15917, A	C 936	196.4	21.7	110266	4	US-09-949-016-18915	Sequence 14915, A
C 864	196.6	21.7	14781	4	US-09-949-016-15917	Sequence 15918, A	C 937	196.4	21.7	110266	4	US-09-949-016-18916	Sequence 14916, A
C 865	196.6	21.7	15108	4	US-09-949-016-11786	Sequence 11786, A	C 938	196.4	21.7	110266	4	US-09-949-016-18917	Sequence 14917, A
C 866	196.6	21.7	15108	4	US-09-949-016-17205	Sequence 117805, A	C 939	196.4	21.7	110266	4	US-09-949-016-18918	Sequence 14918, A
C 867	196.6	21.7	15108	4	US-09-949-016-16380	Sequence 117805, A	C 940	196.4	21.7	110266	4	US-09-949-016-18919	Sequence 14919, A
C 868	196.6	21.7	17488	4	US-09-949-016-15574	Sequence 15574, A	C 941	196.4	21.7	110266	4	US-09-949-016-18920	Sequence 14920, A
C 869	196.6	21.7	18302	4	US-09-949-016-13163	Sequence 15163, A	C 942	196.4	21.7	110266	4	US-09-949-016-18921	Sequence 14921, A
C 870	196.6	21.7	20347	4	US-09-949-016-16752	Sequence 15752, A	C 943	196.4	21.7	110266	4	US-09-949-016-18922	Sequence 14922, A
C 871	196.6	21.7	20942	4	US-09-949-016-15145	Sequence 15149, A	C 944	196.4	21.7	110266	4	US-09-949-016-18923	Sequence 14923, A
C 872	196.6	21.7	20942	4	US-09-949-016-12340	Sequence 12340, A	C 945	196.4	21.7	110266	4	US-09-949-016-18924	Sequence 14924, A
C 873	196.6	21.7	32293	4	US-09-949-016-14203	Sequence 14203, A	C 946	196.4	21.7	110266	4	US-09-949-016-18925	Sequence 14925, A
C 874	196.6	21.7	33155	4	US-09-949-016-16421	Sequence 16421, A	C 947	196.4	21.7	110266	4	US-09-949-016-18926	Sequence 14926, A
C 875	196.6	21.7	33519	4	US-09-949-016-17165	Sequence 17165, A	C 948	196.4	21.7	110266	4	US-09-949-016-18927	Sequence 14927, A
C 876	196.6	21.7	35337	4	US-09-949-016-17249	Sequence 17249, A	C 949	196.4	21.7	131724	4	US-09-949-016-13740	Sequence 13740, A
C 877	196.6	21.7	35337	4	US-09-949-016-16390	Sequence 16390, A	C 950	196.4	21.7	156324	4	US-09-949-016-13747	Sequence 13747, A
C 878	196.6	21.7	36791	4	US-09-949-016-16390	Sequence 16390, A	C 951	196.4	21.7	181251	4	US-09-949-016-13747	Sequence 13747, A
C 879	196.6	21.7	36791	4	US-09-949-016-16390	Sequence 16390, A	C 952	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 880	196.6	21.7	36791	4	US-09-949-016-16390	Sequence 16390, A	C 953	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 881	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 954	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 882	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 955	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 883	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 956	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 884	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 957	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 885	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 958	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 886	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 959	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 887	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 960	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
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C 889	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 962	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
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C 891	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 964	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 892	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 965	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 893	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 966	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 894	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 967	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 895	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 968	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 896	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 969	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 897	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 970	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 898	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 971	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
C 899	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	C 972	196.4	21.7	264665	4	US-09-949-016-13747	Sequence 13747, A
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C 901	196.4	21.7	601	4	US-09-949-016-115947	Sequence 115417, A	C 974	196.2	21.6	32339	4	US-09-949-016-15221	Sequence 15221, A
C 902	196.4	21.7	601	4	US-09-949-016-136815	Sequence 136815, A	C 975	196.2	21.6	32339	4	US-09-949-016-15222	Sequence 15222, A
C 903	196.4	21.7	601	4	US-09-949-016-163105	Sequence 163105, A	C 976	196.2	21.6	32339	4	US-09-949-016-15223	Sequence 15223, A

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981	196.2	21.6	64377	4	US-09-949-016-15212	Sequence 15212, A	c1054	195.8	21.6	601	4	US-09-949-016-122954	Sequence 122954, A
982	196.2	21.6	64377	4	US-09-949-016-15213	Sequence 15213, A	c1055	195.8	21.6	601	4	US-09-949-016-123048	Sequence 123048, A
983	196.2	21.6	64377	4	US-09-949-016-15214	Sequence 15214, A	c1056	195.8	21.6	601	4	US-09-949-016-123142	Sequence 123142, A
984	196.2	21.6	64377	4	US-09-949-016-15215	Sequence 15215, A	c1057	195.8	21.6	601	4	US-09-949-016-123336	Sequence 123336, A
985	196.2	21.6	64377	4	US-09-949-016-15216	Sequence 15216, A	c1058	195.8	21.6	601	4	US-09-949-016-123330	Sequence 123330, A
986	196.2	21.6	72128	4	US-09-949-016-15018	Sequence 15018, A	c1059	195.8	21.6	601	4	US-09-949-016-123372	Sequence 123372, A
987	196.2	21.6	78125	4	US-09-949-016-15006	Sequence 15006, A	c1060	195.8	21.6	601	4	US-09-949-016-123414	Sequence 123414, A
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991	196.2	21.6	87870	4	US-09-949-016-14461	Sequence 14461, A	c1064	195.8	21.6	601	4	US-09-949-016-123582	Sequence 123582, A
992	196.2	21.6	121970	4	US-09-949-016-17216	Sequence 17216, A	c1065	195.8	21.6	601	4	US-09-949-016-123624	Sequence 123624, A
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997	196.2	21.6	134342	4	US-09-949-016-15815	Sequence 15815, A	c1070	195.8	21.6	601	4	US-09-949-016-138596	Sequence 138596, A
998	196.2	21.6	134342	4	US-09-949-016-15815	Sequence 15815, A	c1071	195.8	21.6	601	4	US-09-949-016-195412	Sequence 195412, A
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c1035	196	21.6	78850	4	US-09-949-016-15202	Sequence 15202, A	c1109	195.8	21.6	148405	4	US-09-949-016-12835	Sequence 12835, A
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c1125	195.6	21.6	601	4	US-09-949-016-165010	Sequence 165010,
c1126	195.6	21.6	601	4	US-09-949-016-165019	Sequence 165019,
c1127	195.6	21.6	601	4	US-09-949-016-172869	Sequence 172869,
c1128	195.6	21.6	601	4	US-09-949-016-172887	Sequence 172887,
c1129	195.6	21.6	601	4	US-09-949-016-177642	Sequence 177642,
c1130	195.6	21.6	3198	3	US-09-601-478-3	Sequence 3, Appl1
c1131	195.6	21.6	22368	4	US-09-949-016-15418	Sequence 15418, A
c1132	195.6	21.6	24214	4	US-09-949-016-15551	Sequence 15551, A
c1133	195.6	21.6	30032	4	US-09-949-016-13933	Sequence 13933, A
c1134	195.6	21.6	35676	4	US-09-949-016-13199	Sequence 13199, A
c1135	195.6	21.6	36618	4	US-09-949-016-12861	Sequence 12861, A
c1136	195.6	21.6	38702	4	US-09-949-016-13788	Sequence 13788, A
c1137	195.6	21.6	50217	4	US-09-949-016-16067	Sequence 16067, A
c1138	195.6	21.6	60304	4	US-09-949-016-12218	Sequence 12218, A
c1139	195.6	21.6	60305	4	US-09-949-016-15791	Sequence 15791, A
c1140	195.6	21.6	68719	4	US-09-949-016-12799	Sequence 12799, A
c1141	195.6	21.6	68720	4	US-09-949-016-14296	Sequence 14296, A
c1142	195.6	21.6	98701	4	US-09-949-016-15898	Sequence 15898, A
c1143	195.6	21.6	98701	4	US-09-949-016-15899	Sequence 15899, A
c1144	195.6	21.6	129380	4	US-09-949-016-12544	Sequence 12544, A
c1145	195.6	21.6	135010	4	US-09-949-016-17234	Sequence 17234, A
c1146	195.6	21.6	231129	4	US-09-949-016-16110	Sequence 16110, A
c1147	195.6	21.6	266293	4	US-09-949-016-11934	Sequence 11934, A
c1148	195.6	21.6	387902	4	US-09-949-016-14543	Sequence 14543, A
c1149	195.6	21.6	421883	4	US-09-949-016-12557	Sequence 12557, A
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c1151	195.4	21.5	601	4	US-09-949-016-185141	Sequence 185141,
c1152	195.4	21.5	601	4	US-09-949-016-185173	Sequence 185173,
c1153	195.4	21.5	601	4	US-09-949-016-204057	Sequence 204057,
c1154	195.4	21.5	10103	4	US-09-949-016-11967	Sequence 11967, A
c1155	195.4	21.5	10103	4	US-09-949-016-13245	Sequence 13245, A
c1156	195.4	21.5	11338	4	US-09-949-016-16583	Sequence 16583, A
c1157	195.4	21.5	13883	4	US-09-949-016-15718	Sequence 15718, A
c1158	195.4	21.5	18157	4	US-09-949-016-16193	Sequence 16193, A
c1159	195.4	21.5	20099	4	US-09-949-016-13074	Sequence 13074, A
c1160	195.4	21.5	23051	4	US-09-949-016-16922	Sequence 16922, A
c1161	195.4	21.5	23172	4	US-09-949-016-15161	Sequence 15161, A
c1162	195.4	21.5	32211	4	US-09-949-016-16307	Sequence 16307, A
c1163	195.4	21.5	43333	4	US-09-949-016-15331	Sequence 15331, A
c1164	195.4	21.5	49401	4	US-09-949-016-17080	Sequence 17080, A
c1165	195.4	21.5	49848	4	US-09-949-016-15675	Sequence 15675, A
c1166	195.4	21.5	53332	4	US-09-801-861-3	Sequence 3, Appl1
c1167	195.4	21.5	53332	4	US-10-224-562-3	Sequence 3, Appl1
c1168	195.4	21.5	56551	4	US-09-949-016-12030	Sequence 12030, A
c1169	195.4	21.5	57054	4	US-09-949-016-14159	Sequence 14159, A
c1170	195.4	21.5	57320	4	US-09-949-016-13993	Sequence 13993, A
c1171	195.4	21.5	67366	4	US-09-949-016-16519	Sequence 16519, A
c1172	195.4	21.5	67620	4	US-09-949-016-16939	Sequence 16939, A
c1173	195.4	21.5	76472	4	US-09-949-016-15896	Sequence 15896, A
c1174	195.4	21.5	76610	4	US-09-949-016-15521	Sequence 15521, A
c1175	195.4	21.5	92276	4	US-09-949-016-12166	Sequence 12166, A
c1176	195.4	21.5	102008	4	US-09-949-016-16617	Sequence 16617, A
c1177	195.4	21.5	116592	4	US-09-818-512-3	Sequence 3, Appl1
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c1180	195.4	21.5	150597	4	US-09-949-016-15379	Sequence 15379, A
c1181	195.4	21.5	258449	4	US-09-949-016-17244	Sequence 17244, A
c1182	195.4	21.5	455726	4	US-09-949-016-14157	Sequence 14157, A
c1183	195.4	21.5	481115	4	US-09-949-016-11940	Sequence 11940, A
c1184	195.4	21.5	818128	4	US-09-949-016-14546	Sequence 14546, A
c1185	195.4	21.5	818128	4	US-09-949-016-14547	Sequence 14547, A
c1186	195.4	21.5	818128	4	US-09-949-016-14548	Sequence 14548, A
c1187	195.4	21.5	818128	4	US-09-949-016-14549	Sequence 14549, A
c1188	195.4	21.5	818128	4	US-09-949-016-14550	Sequence 14550, A
c1189	195.4	21.5	818128	4	US-09-949-016-14551	Sequence 14551, A
c1190	195.4	21.5	818128	4	US-09-949-016-14552	Sequence 14552, A
c1191	195.4	21.5	818128	4	US-09-949-016-14553	Sequence 14553, A
c1192	195.4	21.5	818128	4	US-09-949-016-14554	Sequence 14554, A
c1193	195.4	21.5	818128	4	US-09-949-016-14555	Sequence 14555, A
c1194	195.4	21.5	818128	4	US-09-949-016-14556	Sequence 14556, A
c1195	195.4	21.5	818128	4	US-09-949-016-14557	Sequence 14557, A
c1196	195.4	21.5	818128	4	US-09-949-016-14558	Sequence 14558, A
c1197	195.4	21.5	818128	4	US-09-949-016-14559	Sequence 14559, A
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c1202	195.4	21.5	818128	4	US-09-949-016-14564	Sequence 14564, A
c1203	195.4	21.5	818128	4	US-09-949-016-14565	Sequence 14565, A
c1204	195.4	21.5	818128	4	US-09-949-016-14566	Sequence 14566, A
c1205	195.4	21.5	818128	4	US-09-949-016-14567	Sequence 14567, A
c1206	195.2	21.5	601	4	US-09-949-016-29580	Sequence 29580, A
c1207	195.2	21.5	601	4	US-09-949-016-63625	Sequence 63625, A
c1208	195.2	21.5	601	4	US-09-949-016-75729	Sequence 75729, A
c1209	195.2	21.5	601	4	US-09-949-016-148057	Sequence 148057, A
c1210	195.2	21.5	601	4	US-09-949-016-18163	Sequence 18163, A
c1211	195.2	21.5	6647	4	US-09-949-016-103138	Sequence 103138, A
c1212	195.2	21.5	11729	4	US-09-949-016-13247	Sequence 13247, A
c1213	195.2	21.5	25111	4	US-09-949-016-14345	Sequence 14345, A
c1214	195.2	21.5	25111	4	US-09-949-016-13944	Sequence 13944, A
c1215	195.2	21.5	27270	4	US-09-949-016-11822	Sequence 11822, A
c1216	195.2	21.5	27600	4	US-09-949-016-15290	Sequence 15290, A
c1217	195.2	21.5	27923	4	US-09-949-016-13371	Sequence 13371, A
c1218	195.2	21.5	28393	4	US-09-949-016-14980	Sequence 14980, A
c1219	195.2	21.5	31318	4	US-09-949-016-12495	Sequence 12495, A
c1220	195.2	21.5	31319	4	US-09-949-016-15963	Sequence 15963, A
c1221	195.2	21.5	32868	4	US-09-949-016-17406	Sequence 17406, A
c1222	195.2	21.5	33661	4	US-09-949-016-16648	Sequence 16648, A
c1223	195.2	21.5	35060	3	US-08-814-095-7	Sequence 7, Appl1
c1224	195.2	21.5	48018	4	US-09-949-016-17573	Sequence 17573, A
c1225	195.2	21.5	48108	4	US-09-949-016-15555	Sequence 15555, A
c1226	195.2	21.5	48763	4	US-09-949-016-16942	Sequence 16942, A
c1227	195.2	21.5	48763	4	US-09-916-204-3	Sequence 3, Appl1
c1228	195.2	21.5	48763	4	US-10-282-048-3	Sequence 3, Appl1
c1229	195.2	21.5	70014	4	US-09-949-016-17110	Sequence 17110, A
c1230	195.2	21.5	84252	4	US-09-949-016-17315	Sequence 17315, A
c1231	195.2	21.5	113042	4	US-09-949-016-12443	Sequence 12443, A
c1232	195.2	21.5	113042	4	US-09-949-016-15246	Sequence 15246, A
c1233	195.2	21.5	144158	4	US-09-949-016-11755	Sequence 11755, A
c1234	195.2	21.5	144158	4	US-09-949-016-12936	Sequence 12936, A
c1235	195.2	21.5	150409	4	US-09-949-016-12290	Sequence 12290, A
c1236	195.2	21.5	150409	4	US-09-949-016-12338	Sequence 12338, A
c1237	195.2	21.5	323820	4	US-09-949-016-14139	Sequence 14139, A
c1238	195.2	21.5	450395	4	US-09-949-016-15473	Sequence 15473, A
c1239	195.2	21.5	601	4	US-09-949-016-23901	Sequence 23901, A
c1240	195.2	21.5	601	4	US-09-949-016-46249	Sequence 46249, A
c1241	195.2	21.5	601	4	US-09-949-016-89146	Sequence 89146, A
c1242	195.2	21.5	601	4	US-09-949-016-141104	Sequence 141104, A
c1243	195.2	21.5	601	4	US-09-949-016-165186	Sequence 165186, A
c1244	195.2	21.5	601	4	US-09-949-016-166298	Sequence 166298, A
c1245	195.2	21.5	601	4	US-09-949-016-168266	Sequence 168266, A
c1246	195.2	21.5	8096	4	US-09-949-016-12207	Sequence 12207, A
c1247	195.2	21.5	8995	4	US-09-949-016-16214	Sequence 16214, A
c1248	195.2	21.5	97400	4	US-09-949-016-15916	Sequence 15916, A
c1249	195.2	21.5	15033	4	US-09-949-016-16314	Sequence 16314, A
c1250	195.2	21.5	17377	4	US-09-949-016-17331	Sequence 17331, A
c1251	195.2	21.5	23384	4	US-09-949-016-16731	Sequence 16732, A
c1252	195.2	21.5	26867	4	US-09-949-016-16332	Sequence 16333, A
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c1254	195.2	21.5	29327	4	US-09-949-016-14558	Sequence 14558, A
c1255	195.2	21.5	29883	4	US-09-949-016-15885	Sequence 15885, A
c1256	195.2	21.5	29927	4	US-09-949-016-11814	Sequence 11814, A
c1257	195.2	21.5	29927	4	US-09-949-016-17474	Sequence 17474, A
c1258	195.2	21.5	29927	4	US-09-949-016-17475	Sequence 17475, A
c1259	195.2	21.5	30418	4	US-09-949-016-12347	Sequence 12347, A
c1260	195.2	21.5	30418	4	US-09-949-016-14759	Sequence 14759, A
c1261	195.2	21.5	31618	4	US-09-949-016-12639	Sequence 12639, A
c1262	195.2	21.5	37802	4	US-09-949-016-17775	Sequence 17775, A
c1263	195.2	21.5	40130	4	US-09-949-016-13763	Sequence 13763, A
c1264	195.2	21.5	47799	4	US-09-949-016-15753	Sequence 15753, A
c1265	195.2	21.5	49848	4	US-09-949-016-15755	Sequence 15755, A
c1267	195.2	21.5	55298	4	US-09-491-356C-1	Sequence 1, Appl1
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1271	195	21.5	61140	4	US-09-949-016-15771	Sequence 15771, A	1344	194.6	21.5	601	4	US-09-949-016-193121	Sequence 193121,
1272	195	21.5	66219	4	US-09-949-016-12038	Sequence 12038, A	1345	194.6	21.5	601	4	US-09-949-016-193214	Sequence 193214,
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c1275	195	21.5	66227	4	US-09-949-016-15303	Sequence 15303, A	1348	194.6	21.5	10148	4	US-09-949-016-13252	Sequence 13252, A
1276	195	21.5	75395	4	US-09-984-890-3	Sequence 3, App11	c1349	194.6	21.5	15636	4	US-09-949-016-13571	Sequence 13571, A
1277	195	21.5	75395	4	US-10-274-194-3	Sequence 3, App11	1350	194.6	21.5	15636	4	US-09-949-016-18298	Sequence 16298, A
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1280	195	21.5	86213	4	US-09-949-016-17240	Sequence 17240, A	c1353	194.6	21.5	27412	4	US-09-949-016-14329	Sequence 14329, A
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1283	195	21.5	86213	4	US-09-949-016-17243	Sequence 17243, A	c1356	194.6	21.5	43576	4	US-09-949-016-15364	Sequence 15364, A
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c1285	195	21.5	123863	4	US-09-949-016-13453	Sequence 13453, A	c1358	194.6	21.5	49440	4	US-09-949-016-11598	Sequence 14150, A
1286	195	21.5	123863	4	US-09-949-016-14202	Sequence 14202, A	1359	194.6	21.5	50269	4	US-09-949-016-17550	Sequence 17598, A
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1290	194.8	21.5	601	4	US-09-949-016-12427	Sequence 12427, A	1363	194.6	21.5	71651	4	US-09-949-016-11258	Sequence 17073, A
1291	194.8	21.5	601	4	US-09-949-016-180851	Sequence 180851, A	c1364	194.6	21.5	72662	4	US-09-949-016-17073	Sequence 16326, A
1292	194.8	21.5	601	4	US-09-949-016-183999	Sequence 183999, A	c1365	194.6	21.5	73308	4	US-09-949-016-15326	Sequence 15326, A
1293	194.8	21.5	601	4	US-09-949-016-184104	Sequence 184104, A	1366	194.6	21.5	99304	4	US-09-949-016-15440	Sequence 15440, A
1294	194.8	21.5	601	4	US-09-949-016-184209	Sequence 184209, A	1367	194.6	21.5	120727	4	US-09-949-016-15787	Sequence 15787, A
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1296	194.8	21.5	601	4	US-09-949-016-189485	Sequence 189485, A	c1369	194.6	21.5	132438	4	US-09-949-016-13349	Sequence 14339, A
c1297	194.8	21.5	11380	4	US-09-949-016-17172	Sequence 17172, A	c1370	194.6	21.5	132438	4	US-09-949-016-14350	Sequence 14350, A
c1298	194.8	21.5	25769	4	US-09-949-016-17154	Sequence 17154, A	c1371	194.6	21.5	137753	4	US-09-949-016-11404	Sequence 17404, A
c1299	194.8	21.5	29453	4	US-09-949-016-12939	Sequence 12939, A	c1372	194.6	21.5	147440	4	US-09-949-016-15236	Sequence 15236, A
c1300	194.8	21.5	29453	4	US-09-949-016-12940	Sequence 12940, A	c1373	194.6	21.5	151089	4	US-09-949-016-13348	Sequence 14348, A
c1301	194.8	21.5	29453	4	US-09-949-016-12941	Sequence 12941, A	1374	194.6	21.5	524032	4	US-09-949-016-16928	Sequence 16928, A
c1302	194.8	21.5	29453	4	US-09-949-016-12942	Sequence 12942, A	c1375	194.6	21.5	524032	4	US-09-949-016-16928	Sequence 16928, A
c1303	194.8	21.5	31602	4	US-09-949-016-16561	Sequence 16561, A	1376	194.6	21.5	524032	4	US-09-949-016-15929	Sequence 16929, A
c1304	194.8	21.5	36759	4	US-09-949-016-12216	Sequence 12216, A	c1377	194.6	21.5	524032	4	US-09-949-016-16930	Sequence 16930, A
c1305	194.8	21.5	36760	4	US-09-949-016-14021	Sequence 14021, A	1378	194.6	21.5	524032	4	US-09-949-016-16930	Sequence 16930, A
1306	194.8	21.5	38346	4	US-09-949-016-14502	Sequence 14502, A	c1379	194.6	21.5	524032	4	US-09-949-016-16931	Sequence 16931, A
c1307	194.8	21.5	39784	4	US-09-949-016-15128	Sequence 15128, A	c1380	194.6	21.5	524032	4	US-09-949-016-15931	Sequence 16931, A
1308	194.8	21.5	41380	4	US-09-949-016-15128	Sequence 15128, A	c1381	194.6	21.5	524032	4	US-09-949-016-15931	Sequence 16931, A
1309	194.8	21.5	42235	4	US-09-949-016-12558	Sequence 12558, A	1382	194.6	21.5	529685	4	US-09-949-016-13340	Sequence 14340, A
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c1313	194.8	21.5	46682	4	US-09-949-016-17239	Sequence 17239, A	1386	194.6	21.5	529685	4	US-09-949-016-13342	Sequence 14342, A
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c1317	194.8	21.5	51022	4	US-09-949-016-17138	Sequence 17138, A	1390	194.6	21.5	529685	4	US-09-949-016-13344	Sequence 14344, A
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1319	194.8	21.5	78720	4	US-09-949-016-14061	Sequence 14061, A	1392	194.6	21.5	529685	4	US-09-949-016-13345	Sequence 14345, A
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c1321	194.8	21.5	78720	4	US-09-949-016-12783	Sequence 17283, A	1394	194.6	21.5	529685	4	US-09-949-016-13346	Sequence 14346, A
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c1323	194.8	21.5	86213	4	US-09-949-016-17241	Sequence 17241, A	1396	194.6	21.5	529685	4	US-09-949-016-13347	Sequence 14347, A
c1324	194.8	21.5	86213	4	US-09-949-016-17242	Sequence 17242, A	c1397	194.6	21.5	529685	4	US-09-949-016-13347	Sequence 14347, A
c1325	194.8	21.5	86213	4	US-09-949-016-17243	Sequence 17243, A	1398	194.4	21.4	601	4	US-09-949-016-18151	Sequence 18151, A
1326	194.8	21.5	86380	4	US-09-949-016-14637	Sequence 14637, A	c1399	194.4	21.4	601	4	US-09-949-016-105810	Sequence 105810, A
1327	194.8	21.5	87039	4	US-09-949-016-15691	Sequence 15691, A	1400	194.4	21.4	601	4	US-09-949-016-105810	Sequence 105810, A
c1328	194.8	21.5	96987	4	US-09-949-016-14429	Sequence 14429, A	c1401	194.4	21.4	601	4	US-09-949-016-108477	Sequence 108477, A
c1329	194.8	21.5	96987	4	US-09-949-016-17553	Sequence 17553, A	1402	194.4	21.4	601	4	US-09-949-016-109456	Sequence 109456, A
1330	194.8	21.5	112112	4	US-09-949-016-15639	Sequence 15639, A	1403	194.4	21.4	601	4	US-09-949-016-112381	Sequence 112381, A
1331	194.8	21.5	117001	4	US-09-949-016-15684	Sequence 15684, A	1404	194.4	21.4	601	4	US-09-949-016-112689	Sequence 162869, A
1332	194.8	21.5	144596	4	US-09-949-016-11749	Sequence 11749, A	c1405	194.4	21.4	601	4	US-09-949-016-189757	Sequence 189757, A
1333	194.8	21.5	144596	4	US-09-949-016-12733	Sequence 13035, A	c1406	194.4	21.4	601	4	US-09-949-016-201582	Sequence 201582, A
c1334	194.8	21.5	178883	4	US-09-949-016-12733	Sequence 12733, A	1407	194.4	21.4	7070	4	US-09-949-016-12469	Sequence 12469, A
c1335	194.8	21.5	178884	4	US-09-949-016-13039	Sequence 13039, A	1408	194.4	21.4	7070	4	US-09-949-016-13320	Sequence 13320, A
1336	194.8	21.5	250352	4	US-09-949-016-14724	Sequence 14724, A	c1409	194.4	21.4	8150	4	US-09-949-016-13830	Sequence 13830, A
c1337	194.8	21.5	390880	4	US-09-949-016-14720	Sequence 14720, A	1410	194.4	21.4	15927	4	US-09-949-016-12228	Sequence 12228, A
1338	194.6	21.5	304	4	US-09-513-9996-25334	Sequence 25334, A	1411	194.4	21.4	18725	4	US-09-949-016-15977	Sequence 15977, A
c1339	194.6	21.5	601	4	US-09-949-016-51220	Sequence 51220, A	1412	194.4	21.4	34534	4	US-09-949-016-13141	Sequence 15141, A
c1340	194.6	21.5	601	4	US-09-949-016-118217	Sequence 118217, A	1413	194.4	21.4	35104	4	US-09-949-016-15831	Sequence 15831, A
1341	194.6	21.5	601	4	US-09-949-016-158652	Sequence 158652, A	c1414	194.4	21.4	37711	4	US-09-949-016-18232	Sequence 12832, A

c1415	194.4	21.4	37712	4	US-09-949-016-16704	Sequence 16704, A
c1416	194.4	21.4	50368	4	US-09-949-016-13356	Sequence 13236, A
c1417	194.4	21.4	54346	4	US-09-949-016-16206	Sequence 16206, A
c1418	194.4	21.4	63760	4	US-09-949-016-14087	Sequence 14087, A
c1419	194.4	21.4	75312	4	US-09-949-016-13313	Sequence 13313, A
c1420	194.4	21.4	75312	4	US-09-949-016-13314	Sequence 13314, A
c1421	194.4	21.4	75312	4	US-09-949-016-13315	Sequence 13315, A
c1422	194.4	21.4	83462	4	US-09-949-016-15116	Sequence 15116, A
c1423	194.4	21.4	83462	4	US-09-949-016-14736	Sequence 14736, A
c1424	194.4	21.4	87523	4	US-09-949-016-12670	Sequence 12670, A
c1425	194.4	21.4	87523	4	US-09-949-016-15047	Sequence 15047, A
c1426	194.4	21.4	87523	4	US-09-949-016-15048	Sequence 15048, A
c1427	194.4	21.4	87523	4	US-09-949-016-15049	Sequence 15049, A
c1428	194.4	21.4	87869	4	US-09-949-016-11744	Sequence 11744, A
c1429	194.4	21.4	87869	4	US-09-949-016-15044	Sequence 15044, A
c1430	194.4	21.4	87869	4	US-09-949-016-15045	Sequence 15045, A
c1431	194.4	21.4	87869	4	US-09-949-016-15046	Sequence 15046, A
c1432	194.4	21.4	100836	4	US-09-949-016-12871	Sequence 12871, A
c1433	194.4	21.4	100836	4	US-09-949-016-17063	Sequence 17063, A
c1434	194.4	21.4	118136	4	US-09-949-016-12439	Sequence 12439, A
c1435	194.4	21.4	194937	4	US-09-949-016-17032	Sequence 17032, A
c1436	194.4	21.4	194937	4	US-09-949-016-17033	Sequence 17033, A
c1437	194.4	21.4	228851	4	US-09-949-016-13781	Sequence 13781, A
c1438	194.4	21.4	260247	4	US-09-949-016-13358	Sequence 13358, A
c1439	194.4	21.4	260247	4	US-08-579-445-26	Sequence 26, Appl
c1440	194.2	21.4	283	4	US-09-949-016-58582	Sequence 58582, A
c1441	194.2	21.4	601	4	US-09-949-016-60226	Sequence 60226, A
c1442	194.2	21.4	601	4	US-09-949-016-60227	Sequence 60227, A
c1443	194.2	21.4	601	4	US-09-949-016-60227	Sequence 60227, A
c1444	194.2	21.4	601	4	US-09-949-016-96520	Sequence 96520, A
c1445	194.2	21.4	601	4	US-09-949-016-96786	Sequence 96786, A
c1446	194.2	21.4	601	4	US-09-949-016-97052	Sequence 97052, A
c1447	194.2	21.4	601	4	US-09-949-016-97318	Sequence 97318, A
c1448	194.2	21.4	601	4	US-09-949-016-97584	Sequence 97584, A
c1449	194.2	21.4	601	4	US-09-949-016-97850	Sequence 97850, A
c1450	194.2	21.4	601	4	US-09-949-016-98116	Sequence 98116, A
c1451	194.2	21.4	601	4	US-09-949-016-98382	Sequence 98382, A
c1452	194.2	21.4	601	4	US-09-949-016-98648	Sequence 98648, A
c1453	194.2	21.4	601	4	US-09-949-016-98914	Sequence 98914, A
c1454	194.2	21.4	601	4	US-09-949-016-99180	Sequence 99180, A
c1455	194.2	21.4	601	4	US-09-949-016-99446	Sequence 99446, A
c1456	194.2	21.4	601	4	US-09-949-016-99712	Sequence 99712, A
c1457	194.2	21.4	601	4	US-09-949-016-99978	Sequence 99978, A
c1458	194.2	21.4	601	4	US-09-949-016-100244	Sequence 100244, A
c1459	194.2	21.4	601	4	US-09-949-016-100510	Sequence 100510, A
c1460	194.2	21.4	601	4	US-09-949-016-100776	Sequence 100776, A
c1461	194.2	21.4	601	4	US-09-949-016-101080	Sequence 101080, A
c1462	194.2	21.4	601	4	US-09-949-016-101346	Sequence 101346, A
c1463	194.2	21.4	601	4	US-09-949-016-101612	Sequence 101612, A
c1464	194.2	21.4	601	4	US-09-949-016-101878	Sequence 101878, A
c1465	194.2	21.4	601	4	US-09-949-016-102298	Sequence 102298, A
c1466	194.2	21.4	601	4	US-09-949-016-102438	Sequence 102438, A
c1467	194.2	21.4	601	4	US-09-949-016-132868	Sequence 132868, A
c1468	194.2	21.4	601	4	US-09-949-016-139110	Sequence 139110, A
c1469	194.2	21.4	601	4	US-09-949-016-143344	Sequence 143344, A
c1470	194.2	21.4	601	4	US-09-949-016-143515	Sequence 143515, A
c1471	194.2	21.4	601	4	US-09-949-016-154653	Sequence 154653, A
c1472	194.2	21.4	601	4	US-09-949-016-186006	Sequence 186006, A
c1473	194.2	21.4	4428	4	US-09-023-655-1109	Sequence 1109, Ap
c1474	194.2	21.4	8165	4	US-09-949-016-16816	Sequence 16816, A
c1475	194.2	21.4	9157	4	US-09-949-016-16185	Sequence 16185, A
c1476	194.2	21.4	14961	4	US-09-949-016-13400	Sequence 13400, A
c1477	194.2	21.4	15084	4	US-09-949-016-16277	Sequence 16277, A
c1478	194.2	21.4	20674	3	US-09-641-638-651	Sequence 651, App
c1479	194.2	21.4	20674	4	US-10-097-651	Sequence 651, App
c1480	194.2	21.4	35688	4	US-09-949-016-16873	Sequence 16873, A
c1481	194.2	21.4	37269	4	US-09-949-016-16672	Sequence 16672, A
c1482	194.2	21.4	41613	4	US-09-949-016-16125	Sequence 16125, A
c1483	194.2	21.4	43657	4	US-09-949-016-13777	Sequence 13777, A
c1484	194.2	21.4	57875	4	US-09-949-016-13152	Sequence 13152, A
c1485	194.2	21.4	63187	4	US-09-949-016-12682	Sequence 12682, A
c1486	194.2	21.4	63187	4	US-09-949-016-16288	Sequence 16288, A
c1487	194.2	21.4	84425	4	US-09-949-016-17402	Sequence 17402, A

RESULT 1
US-09-949-016-14632
Sequence 14632, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14632
LENGTH: 12445
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(12445)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14632

Query Match 99.8%; Score 905.4; DB 4; Length 12445;
Best Local Similarity 99.8%; Pred. No. 1.7e-271;
Matches 906; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GGACTGTGAAGTCCGACAGCTGCTGAGGCCGCCAGAGAGTGTTCACCTTGGAC	60
DB	11182	GAGCTGTGAAGTCCGACAGCTGCTGAGGCCGCCAGAGAGTGTTCACCTTGGAC	11241
QY	61	CCCTAGGGGTCTGATTTGCTGTGTTAAAGATTAACCTAGGCGAGACCCATAGGGGA	120
DB	11242	CCCTAGGGGTCTGATTTGCTGTGTTAAAGATTAACCTAGGCGAGACCCATAGGGGA	11301
QY	121	AGTCTACCTCTCGGCTCCCTGACCTGCTGATTCAGCGTGGCTGTCTCTTGGC	180
DB	11302	ATGCTACCTCTCGGCTCCCTGACCTGCTGATTCAGCGTGGCTGTCTCTTGGC	11361
QY	181	GAGAGAGTCTCTGGGTCAAGGACGAGAGAGAGCTTCAAGACTCAAGCCCTTGTACC	240
DB	11362	GAGAGAGTCTCTGGGTCAAGGACGAGAGAGAGCTTCAAGACTCAAGCCCTTGTACC	11421
QY	241	GAGAGAGACTTGGCAAGTTCAGCGATGCTCCGAGTCCACACAGATGGCGGACG	300
DB	11422	GAGAGAGACTTGGCAAGTTCAGCGATGCTCCGAGTCCACACAGATGGCGGACG	11481
QY	301	GGAGAGGGGGGACAGTTCTGTGTGCTGTGGATGAGACATTAAGAGGCTTGGCACTCA	360

Db	11482	GCAGAGGGGGGACA	GTTCCTGTTGTGCTTGGTTGGACAGTAAAGAGGGTCTTGGCCAGTCCA	11541
Qy		GGGTGGGGGGGGG	CAAACTCCATTAAGAAACGAGGGGTCTGGGCCCCGCGCACAGAGTCA	420
Db	11542	GGGTGGGGGGGGG	CAAACTCCATTAAGAAACGAGGGGTCTGGGGCCCCGCGCACAGAGTCA	11601
Qy		TCCTGGCCAGCTC	CTCTGCTGCTGGCCAGTGGGAGTGGCAGAGGTGGGGCTTTGTGTCCAG	480
Db	11602	TCCTGGCCAGCTC	CTCTGCTGCTGGCCAGTGGGAGTGGCAGAGGTGGGGCTTTGTGTCCAG	11661
Qy		481	TAAACCAACAAGCTGGAATTTGCTCGCGGCATGTGCTCCCTGCTTAAAGGAGCAATTTCTCA	540
Db	11662	TAAACCAACAAGCTGGAATTTGCTCGCGGCATGTGCTCCCTGCTTAAAGGAGCAATTTCTCA		11721
Qy		541	ACCTTCTTGTCTCAAGAACCCCAAGAGCTTTCAATTGATCTAATGATTTTAAACAATTT	600
Db	11722	ACCTTCTTGTCTCAAGAACCCCAAGAGCTTTCAATTGATCTAATGATTTTAAACAATTT		11781
Qy		601	AGCAATTAAACTGAGAAATGGGGCGGGGACGGTGGCTACGCTGTAATCCAGACTT	660
Db	11782	AGCAATTAAACTGAGAAATGGGGCGGGGACGGTGGCTACGCTGTAATCCAGACTT		11841
Qy		661	TGGGAGCGCGAGGCGGGTGGATCACTTGAGATCAGAGATTCAAGACCAAGCTTGGCCAACT	720
Db	11842	TGGGAGCGCGAGGCGGGTGGATCACTTGAGATCAGAGATTCAAGACCAAGCTTGGCCAACT		11901
Qy		721	TGTGTAAACCTTGTCTACTTAAATAATACAAATAATTACGACGACACAGTGGTGTGCACTGG	780
Db	11902	TGTGTAAACCTTGTCTACTTAAATAATACAAATAATTACGACGACACAGTGGTGTGCACTGG		11961
Qy		781	TAGTCCCACTTAATCTGGGAGGCTGAGGCGCAGAAATCGCTTGAACCCAGAGGCGGACGT	840
Db	11962	TAGTCCCACTTAATCTGGGAGGCTGAGGCGCAGAAATCGCTTGAACCCAGAGGCGGACGT		12021
Qy		841	TGCGGTGAGCGGAGATCGCGCCGCTGATTCAGACCTGCGCGCACAAGATGAGACTCCATC	900
Db	12022	TGCGGTGAGCGGAGATCGCGCCGCTGATTCAGACCTGCGCGCACAAGATGAGACTCCATC		12081
Qy		901	TCACACA	907
Db	12082	TCACACA	12088	
RESULT 2				
US-09-949-016-15748				
; Sequence 15748, Application US/09949016				
; Patent No. 6812339				
; GENERAL INFORMATION:				
; APPLICANT: VENTER, J. Craig et al.				
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED				
; FILE REFERENCE: C1001307				
; CURRENT APPLICATION NUMBER: US/09/949, 016				
; PRIORITY FILING DATE: 2000-04-14				
; PRIOR APPLICATION NUMBER: 60/241,755				
; PRIOR FILING DATE: 2000-10-20				
; PRIOR APPLICATION NUMBER: 60/237,768				
; PRIOR FILING DATE: 2000-10-03				
; PRIOR APPLICATION NUMBER: 60/231,498				
; PRIOR FILING DATE: 2000-09-08				
; NUMBER OF SEQ ID NOS: 207012				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 15748				
; LENGTH: 21691				
; TYPE: DNA				
; ORGANISM: Human				
; FEATURE:				
; NAME/KEY: misc_feature				
; LOCATION: (1)...(21691)				
; OTHER INFORMATION: n = A,T,C or G				
US-09-949-016-15748				
Query Match	99.8%	Score 905.4	DB 4	Length 21691

		Best Local Similarity 99.9%; Pred.No.2.2e-271.										
		Matches 906; Conservative 0; Mismatches 1; Indels 0; Gaps 0;										
QY	1	GGA	CTGTAAAGGTC	CCAGACAGCTGCTGAGGCC	CCAGAGAAAGTGTTC	CAACCTTGGAC	60					
Db	11165	GA	CTCTGAAGGTC	CCAGACAGCTGCTGAGGCC	CCCAAGAAAGTGTTC	CAACCTTGGAC	11224					
QY	61	CCCTA	GGGGGCTG	GAATTTGCTGT	TAAACAAGATAC	CTAAGGGCAGGAC	CCCATATGGGG	120				
Db	11225	CCCTA	GGGGGCTG	GAATTTGCTGT	TAAACAAGATAC	CTAAGGGCAGGAC	CCCATATGGGG	11284				
QY	121	ATG	CTACTCTTCG	CCCTTCCACCTG	CCCTGTGTTCACCG	GTGGCCCTGT	CCTCTTGGC	180				
Db	11285	ATG	CTACTCTTCG	CCCTTCCACCTG	CCCTGTGTTCACCG	GTGGCCCTGT	CCTCTTGGC	11344				
QY	181	GAG	AGAGTGTCT	TGGGTCAAGG	ACGCAAGACGCTCA	CAGACTCAAG	CCCTTGTACC	240				
Db	11345	GAG	AGAGTGTCT	TGGGTCAAGG	ACGCAAGACGCTCA	CAGACTCAAG	CCCTTGTACC	11404				
QY	241	GAA	AGACACCTT	GGCAGAGTCC	AGCGCATGGTCCG	AGTCCACACACAG	CTGGCCGACG	300				
Db	11405	GAA	AGACACCTT	GGCAGAGTCC	AGCGCATGGTCCG	AGTCCACACACAG	CTGGCCGACG	11464				
QY	301	GCA	GAGAGGGG	GAGCAGTTCT	GTGTGGTTGGACAGT	AAAGAGGTCTT	TGGCCAGTCCA	360				
Db	11465	GCA	GAGAGGGG	GAGCAGTTCT	GTGTGGTTGGACAGT	AAAGAGGTCTT	TGGCCAGTCCA	11524				
QY	361	GGG	TGGGGGGCGG	CAAACTTC	CAATPAAGAAC	CAAGAGGTCT	TGGGCCCCCGGCC	CAAGAGTCA	420			
Db	11525	GGG	TGGGGGGCGG	CAAACTTC	CAATPAAGAAC	CAAGAGGTCT	TGGGCCCCCGGCC	CAAGAGTCA	11584			
QY	421	TC	TGCCCAAGT	CCTCTCTGCTG	GGCCAGTGGAGTGG	CAACAGAGTGGGGCTT	TGGGCCAG	480				
Db	11585	TC	TGCCCAAGT	CCTCTCTGCTG	GGCCAGTGGAGTGG	CAACAGAGTGGGGCTT	TGGGCCAG	11644				
QY	481	TAA	AAACCA	CAGCGCTG	ATTTGCTCGCGGGCC	CAATGTCCTCTGT	CTAAGGGCAG	CAATTCTCA	540			
Db	11645	TAA	AAACCA	CAGCGCTG	ATTTGCTCGCGGGCC	CAATGTCCTCTGT	CTAAGGGCAG	CAATTCTCA	11704			
QY	541	ACC	TTCTTGCTCT	CAGGACCC	CAAGAGCTTTCAT	TGTAATCTA	TGTGATTTTAC	CACATTT	600			
Db	11705	ACC	TTCTTGCTCT	CAGGACCC	CAAGAGCTTTCAT	TGTAATCTA	TGTGATTTTAC	CACATTT	11764			
QY	601	AG	CAATTA	AAACCTG	GAAGAAATGG	GGCCCGGGC	ACGCTGCTCA	CGCCTGTAT	TCCACAGACTT	660		
Db	11765	AG	CAATTA	AAACCTG	GAAGAAATGG	GGCCCGGGC	ACGCTGCTCA	CGCCTGTAT	TCCACAGACTT	11824		
QY	661	TGG	AGAGCG	CGAGCGGG	TGGATCACTCT	GAGATCAGG	AGTTCAAGAC	CAAGAC	CAAGCTTGGCC	CAACA	720	
Db	11825	TGG	AGAGCG	CGAGCGGG	TGGATCACTCT	GAGATCAGG	AGTTCAAGAC	CAAGAC	CAAGCTTGGCC	CAACA	11884	
QY	721	TGG	TGA	AAACCTTGTCT	TACTAATAA	AAATNCA	AAAAATTN	AGCAGG	CA	CAGTGTGTGCA	CTGG	780
Db	11885	TGG	TGA	AAACCTTGTCT	TACTAATAA	AAATNCA	AAAAATTN	AGCAGG	CA	CAGTGTGTGCA	CTGG	11944
QY	781	TAG	TCCCA	GTTATCTCG	GAGAGGCTG	AGGACAG	AAAAATCG	CTTGA	ATCC	CAAGAGAGCG	CGACCT	840
Db	11945	TAG	TCCCA	GTTATCTCG	GAGAGGCTG	AGGACAG	AAAAATCG	CTTGA	ATCC	CAAGAGAGCG	CGACCT	12004
QY	841	TGG	GGTGA	GCGCGAG	ATCGCGCGCTG	ATTTCCAG	CCCTGGGCG	CA	CAAG	AGTGA	ACTTCATTC	900
Db	12005	TGG	GGTGA	GCGCGAG	ATCGCGCGCTG	ATTTCCAG	CCCTGGGCG	CA	CAAG	AGTGA	ACTTCATTC	12064
QY	901	TC	A	CACACA	907							
Db	12065	TC	A	CACACA	12071							
RESULT 3												
US-09-799-451-204												
Sequence 204, Application US/09799451												
Patent No. 6783969												
GENERAL INFORMATION:												

Db 61 TCAGGACGACAGAGACGCTCACAGACTCCAGCCCTTTTACCGAGAGGACATTGGCA 120
QY 257 AGGTCCAGGATGATGTCGAGATCCACACAGACTGGCCGACAGAGGGGGACAGT 316
Db 121 AGGTCCAGGATGATGTCGAGATCCACACAGACTGGCCGACAGAGGGGGACAGT 180
QY 317 TCGTGTGCTGCTGTTGAGACAGTAAGAGGATCTTGGACAGTCCAGGGTGGGGGGGCA 376
Db 181 TCGTGTGCTGCTGTTGAGACAGTAAGAGGATCTTGGCCAGTCCAGGGTGGGGGGGCA 240
QY 377 ACTCATTAAGAACAGAGGATCTGGGCCCGGACAGAGTATCTGCCAGCTCTCT 436
Db 241 ACTCATTAAGAACAGAGGATCTGGGGCCCGGACAGAGTATCTGCCAGCTCTCT 300
QY 437 GCTGCTGGCCAGTGGAGATGGCACAGAGTGGGGCTTTGGCCAGTAACCAAGCTGG 496
Db 301 GCTGCTGGCCAGTGGAGATGGCACAGAGTGGGGCTTTGGCCAGTAACCAAGCTGG 360
QY 497 ATTGCTGGGGGACAGAGTCCCTGTCTAGGGGACAAATTCAGCCTTCTGCTCTAG 556
Db 361 ATTGCTGGGGGACAGAGTCCCTGTCTAGGGGACAAATTCAGCCTTCTGCTCTAG 420
QY 557 GACCCCAAGAGCTTCAATTGATCTATTGATTTTACCAATTAGCAATTAAGCTGAG 616
Db 421 GACCCCAAGAGCTTCAATTGATCTATTGATTTTACCAATTAGCAATTAAGCTGAG 480
QY 617 AATGGGCGGGGACAGCTGG 636
Db 481 AATGGGCGGGGACAGCTGG 500

RESULT 5
US-09-949-016-16514/C
; Sequence 16514, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16514
; LENGTH: 160759
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(160759)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16514

Query Match 23.4%; Score 211.8; DB 4; Length 160759;
Best Local Similarity 84.0%; Pred. No. 1,4e-54;
Matches 263; Conservative 0; Mismatches 47; Indels 3; Gaps 2;

QY 598 ATTAGCAATTAAATCGAAGAAATGGCCCGGACAGGCTGCTCAGCCTGTAATCCAGCA 657
Db 68534 ATGATATAATTATTAATAGCCTTAAGGCTGGGACAGGCTGCTCAGCCTGTAATCCAGCA 68475
QY 658 CTTTGGAGCGGACGCGGCTGATCACTTGAGATCAAGAGTTCAAGACCAAGCTGGCCA 717
Db 68474 CTTTGGAGCGGACGCGGCTGATCACTTGAGATCAAGAGTTCAAGACCAAGCTGGCCA 68415
QY 718 ACATGCTGA--CTTGTCTACTAAATAATCAAAAAATTAGCCAGGACAGTGTGTGC 775

Db 68414 ACATGCTGAATCCGCTCTACTTAATAATAATAATTAACCAAGCTTGTGTGTGC 68355
QY 776 ACTGTAATGCCAGTTACTTCGGAGGCTGAGGACAGAAATGCTTTGAACCCAGAGAGCG 835
Db 68354 ACTGTAATGCCAGTTACTTCGGAGGCTGAGGACAGAAATGCTTTGAACCCAGAGAGCG 68295
QY 836 GACGTTGGGAGGACGAGATGCGCGCTG-ATTCCAGCTTGGGACAGAGTGAAG 894
Db 68294 GAGGTTGACGTAAACATGATGCGCCACAGACCTCCAGCTGGGACAGAGTGAAC 68235
QY 895 TCCATCTCACACA 907
Db 68234 TTTGTCTCAAAAA 68222

RESULT 6
US-09-949-016-15377
; Sequence 15377, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15377
; LENGTH: 23533
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15377

Query Match 23.3%; Score 211.2; DB 4; Length 23533;
Best Local Similarity 78.5%; Pred. No. 7.6e-55;
Matches 278; Conservative 0; Mismatches 73; Indels 3; Gaps 2;

QY 557 GACCCCAAGAGCTTCAATTGATCTATTGATTTTACCACTTGAATTAAGCTGAG 616
Db 5478 GAGACCATGATGAGAGCAATAGATGACGAGACCCCATCTCTTAATAAAAAA 5537
QY 617 AATGGGCGGGACAGGATGCTCAGCCTGTAATCCAGCACTTTGGAGGCGGAGCG 676
Db 5538 AAAAAAGCGGGACAGGATGCTCAGCCTGTAATCCAGCACTTTGGAGGCGGAGCG 5597
QY 677 GTGATCACTGATGATCAAGAGTTCAAGACAGCCTGGCCAAATGTGAAACTTGT-- 734
Db 5598 GCAATCACTGATGATGAGGATTTGAAGACAGCCTGGCCAAATGTGAAACTTGTCC 5657
QY 735 CTACTAAATAATCAAAAAATTGACAGGACAGTGTGTGACCTGTAGTCCAGTACT 794
Db 5658 CTACTAAATAATCAAAAAATTGAGGATGAGTGTGTGACCTGTAGTCCAGTACT 5717
QY 795 CGGAGGCTGAGGACAGAAATCGCTGAACCCAGAGGCGGACGTTGGGTGAGCGGAG 854
Db 5718 CGGAGGCTGAGGACAGAAATCAATTGAACCCAGAGGCGGATTTGAGATGAGCGGAG 5777
QY 855 ATCGCGCGCTG-ATTCCAGCTTGGGCGCAAGAGTGAATCTCAATTCTCACACA 907
Db 5778 ATCGCGCGCTGATCTCAAGCTTGGGGGACAAAGAGGAGACTTCAATCTCAAAA 5831

RESULT 7
US-09-949-016-12969
; Sequence 12969, Application US/09949016

```

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12969
; LENGTH: 36148
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12969

```

```

Query Match      23.2%; Score 210.6; DB 4; Length 36148;
Best Local Similarity 84.7%; Pred. No. 1.5e-54;
Matches 260; Conservative 0; Mismatches 44; Indels 3; Gaps 2;

```

```

QY 604 AATTAAACTGAGAAATGGGCGCGGCGCTGCTGATCTGATCCAGCACTTTGG 663
DB 15312 AATTAAGAGAAACCTTGGCCCGGCGATGCTGCTGATCCAGCACTTTGG 15371
QY 664 GAGCGCGAGCGGCGGCTGATCCTGATGATGAGATGAGATGAGATGAGATG 723
DB 15372 GAGCGCGAGCGGCGGCTGATCCTGATGATGAGATGAGATGAGATGAGATG 15431
QY 724 TGAACCTTG--TCTACTAATAATATCAAAATTAAGCAGGACAGGCTGATGATG 781
DB 15432 CAAGACCTGCTCTCTACTAATAATAATTAAGCAGGCTGATGATGATGATGATG 15491
QY 782 AGTCCAGCTTACTCGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 841
DB 15492 AATCCAGCTTACTCGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 15551
QY 842 GCGGTGAGCGGAGATCGCGCGCTG--ATTCCAGCTGCGGAGGAGGAGGAGGAGG 900
DB 15552 GCGGTGAGCGGAGATCGCGCGCTGATCTCAAGCTGCGGAGGAGGAGGAGGAGG 15611
QY 901 TCACACA 907
DB 15612 TCAAAA 15618

```

```

RESULT 8
US-09-949-016-11957/c
; Sequence 11957, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11957
; LENGTH: 64813
; TYPE: DNA

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; ORGANISM: Human
; US-09-949-016-11957

```

```

Query Match      23.2%; Score 210.6; DB 4; Length 64813;
Best Local Similarity 80.2%; Pred. No. 2e-54;
Matches 272; Conservative 0; Mismatches 64; Indels 3; Gaps 2;

```

```

QY 572 TCATTGTATCTATTGATTTTACACATTAAGCAATTAAGCAATTAAGCAATTAAGCA 631
DB 17739 TCAATTTTCACTAATCAATTTTATTAATTAATTAATTAATTAATTAATTAATTA 17680
QY 632 GGTGCTCAGCGCTGATATCCAGCACTTTGGAGGCGGAGGCGGCTGATCCTGAGA 691
DB 17679 GGTAGCTCAGCGCTGATATCCAGCACTTTGGAGGCTGAGGCGGCTGATCCTGAGA 17620
QY 692 TCAGAGTTCAAGACCAAGCTGCGCAATGTTGAA--CTTTGTACTTAATAATTAACA 749
DB 17619 TCAGAGTTCAAGACCAAGCTGCGCAATGTTGAA--CTTTGTACTTAATAATTAACA 17560
QY 750 AATTTAGCCAGGACAGTGTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 809
DB 17559 AATTTAGCCAGGACAGTGTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 17500
QY 810 GGAATTCGCTTGAACCCAGAGGCGGAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAG 868
DB 17499 GGAATTCGCTTGAACCCAGAGGCGGAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAG 17440
QY 869 TCCAGCTTGGCGGAGCAAGATGAGTCAATCTCACA 907
DB 17439 TCCAGCTTGGCGGAGCAAGATGAGTCAATCTCACA 17401

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```

RESULT 9
US-09-949-016-16064/c
; Sequence 16064, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16064
; LENGTH: 70131
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16064

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```

Query Match      23.2%; Score 210.6; DB 4; Length 70131;
Best Local Similarity 80.2%; Pred. No. 2.1e-54;
Matches 272; Conservative 0; Mismatches 64; Indels 3; Gaps 2;

```

```

QY 572 TCATTGTATCTATTGATTTTACACATTAAGCAATTAAGCAATTAAGCAATTAAGCA 631
DB 23393 TCAATTTTCACTAATCAATTTTATTAATTAATTAATTAATTAATTAATTAATTA 23334
QY 632 GGTGCTCAGCGCTGATATCCAGCACTTTGGAGGCGGAGGCGGCTGATCCTGAGA 691
DB 23333 GGTAGCTCAGCGCTGATATCCAGCACTTTGGAGGCTGAGGCGGCTGATCCTGAGA 22274
QY 692 TCAGAGTTCAAGACCAAGCTGCGCAATGTTGAA--CTTTGTACTTAATAATTAACA 749
DB 23373 TCAGAGTTCAAGACCAAGCTGCGCAATGTTGAA--CTTTGTACTTAATAATTAACA 23214

```

```

QY 750 AAAATTAGCCAGGACAGTGTGTGACCTGATCCAGTTACTGCGAGGCTGAGGAC 809
  |||||
Db 23213 AAAATTGGCCGGGACATGTTGGGGGTTCTGTGTAATCCGCTAATTGGAGGCTGAGGCA 23154
  |||||
QY 810 GGAATAATCGCTTGAACCCAGAGGCGGAGCGTTGCGGTGAGCCGAGATCGCGCGCTG-AT 868
  |||||
Db 23153 GGAGATCACTTGACCTGGAGGCGAGAGGTTGACATGAGCCGAGATTGCACTGACCTGAAC 23094
  |||||
QY 869 TCCAGCTTGGGCGACAAAGTGTGAGATCCATCTCACACA 907
  |||||
Db 23093 TCCAACTGAGCAACAAGAGTGAATCCATCTCAAAAA 23055
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```

RESULT 10

US-09-949-016-12682
; Sequence 12682, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12682

LENGTH: 63187

TYPE: DNA

ORGANISM: Human

US-09-949-016-12682

Query Match

Best Local Similarity 82.9%; Score 210.4; DB 4; Length 63187;

Matches 252; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

```

QY 605 ATTAAATGAGAAATGGCGCGGACGCTGCTCAGCCTGTAAATCCAGCACTTTGGG 664
  |||||
Db 8887 ATTAAGTATATAGCTGTGGCCGGGACGCTGCTTAAGCTAATCCAGCACTTTGGG 8946
  |||||
QY 665 AGCCGAGCGGGGTGATCAGCTGAGATGAGATCAAGACCAAGCTGCGCAACATGGT 724
  |||||
Db 8947 AGCTGAGCGGGGTGATCAGCTGAGATGAGATCAAGACCAAGCTGCGCAACATGGT 9006
  |||||
QY 725 GAAACCTTGTCTAATAAATTAACAAATTTAGCCAGGACAGTGTGTGCACTGTACT 784
  |||||
Db 9007 GAAACCCCTCTAATAAATTAACAAATTTAGTGGCATGTGTGCACTGTGTAAAT 9066
  |||||
QY 785 CCCAGTTACTCGGAGGCTGAGGACGAGAAATCGCTTGAACCAAGAGGCGGACGTTGGG 844
  |||||
Db 9067 CCCAGTTACTCGGAGGCTGAGGACGAGAAATCAATGAACCCGTAGCCAGAGGTTGCA 9126
  |||||
QY 845 GTGAGCCGAGATCGCGCGCTG-ATTCCAGCTTGGGCGCAAGAGTGAATCCATCTCA 903
  |||||
Db 9127 GTGAGCCAGAAATTGTGCCACTGCAATTCAGCCTGGGCGCAAGAGTGAATCTGTCTCA 9186
  |||||
QY 904 CACA 907
  |||||
Db 9187 AAAA 9190
  |||||

```

RESULT 11

US-09-949-016-16288

; Sequence 16288, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16288
; LENGTH: 63187
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16288

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Query Match

Best Local Similarity 82.9%; Score 210.4; DB 4; Length 63187;

Matches 252; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

```

QY 605 ATTAAATGAGAAATGGCGCGGACGCTGCTCAGCCTGTAAATCCAGCACTTTGGG 664
  |||||
Db 8887 ATTAAGTATATAGCTGTGGCCGGGACGCTGCTTAAGCTAATCCAGCACTTTGGG 8946
  |||||
QY 665 AGCCGAGCGGGGTGATCAGCTGAGATGAGATCAAGACCAAGCTGCGCAACATGGT 724
  |||||
Db 8947 AGCTGAGCGGGGTGATCAGCTGAGATGAGATCAAGACCAAGCTGCGCAACATGGT 9006
  |||||
QY 725 GAAACCTTGTCTAATAAATTAACAAATTTAGCCAGGACAGTGTGTGCACTGTACT 784
  |||||
Db 9007 GAAACCCCTCTAATAAATTAACAAATTTAGTGGCATGTGTGCACTGTGTAAAT 9066
  |||||
QY 785 CCCAGTTACTCGGAGGCTGAGGACGAGAAATCGCTTGAACCAAGAGGCGGACGTTGGG 844
  |||||
Db 9067 CCCAGTTACTCGGAGGCTGAGGACGAGAAATCAATGAACCCGTAGCCAGAGGTTGCA 9126
  |||||
QY 845 GTGAGCCGAGATCGCGCGCTG-ATTCCAGCTTGGGCGCAAGAGTGAATCCATCTCA 903
  |||||
Db 9127 GTGAGCCAGAAATTGTGCCACTGCAATTCAGCCTGGGCGCAAGAGTGAATCTGTCTCA 9186
  |||||
QY 904 CACA 907
  |||||
Db 9187 AAAA 9190
  |||||

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RESULT 12

US-09-949-016-12786/C

; Sequence 12786, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12786

LENGTH: 35678

TYPE: DNA

ORGANISM: Human

US-09-949-016-12786


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Query Match      23.1%; Score 209.2; DB 4; Length 35678;
Best Local Similarity 79.7%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 598 ATTAGCAATTAAACTGAGAAATGGCGCGGCGGCGCTGATCCAGCTGTAATCCCGACA 657
DB 10261 ATATGTAATTAAATAATATAGAGACGCTGGCACAGTGCTTATGCTTATATATCCACGA 10202

QY 658 CTTTGGAGGCGCGAGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCTGGCCA 717
DB 10201 CTTTGGAGGCGCGAGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCTGGCCA 10142

QY 718 ACATGGTGAACCTTGTCTACTAATAAAATTAACCAAGGCAAGTGTGTGCAC 777
DB 10141 ACATGGTGAACCTTGTCTACTAATAAAATTAACCAAGGCAAGTGTGTGCAC 10082

QY 778 TGGTAGTCCCACTTACTCTGGGAGGCTGAGGCAAGAAAATGCTTGAACCCAGAGGCGGA 837
DB 10081 CTATTAATCCCACTTACTCTGGGAGGCTGAGGCAAGAAAATGCTTGAACCCAGAGGCGGA 10022

QY 838 CGTTGGCGGTAGCGAGATGCGCGCGCTGATTCCAGCGCTGGCGACAAGATGAGACTCC 897
DB 10021 GGTTCAGTAGTGAATGAGATCAAGCCACTGCACTCCAGCTGGGTGAGAGTCAAGTCTT 9962

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

RESULT 13
US-09-949-016-16757/c
; Sequence 16757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16757
; LENGTH: 35678
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16757

Query Match      23.1%; Score 209.2; DB 4; Length 35678;
Best Local Similarity 79.7%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 598 ATTAGCAATTAAACTGAGAAATGGCGCGGCGGCGCTGATCCAGCTGTAATCCCGACA 657
DB 10261 ATATGTAATTAAATAATATAGAGACGCTGGCACAGTGCTTATGCTTATATATCCACGA 10202

QY 658 CTTTGGAGGCGCGAGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCTGGCCA 717
DB 10201 CTTTGGAGGCGCGAGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCTGGCCA 10142

QY 718 ACATGGTGAACCTTGTCTACTAATAAAATTAACCAAGGCAAGTGTGTGCAC 777
DB 10141 ACATGGTGAACCTTGTCTACTAATAAAATTAACCAAGGCAAGTGTGTGCAC 10082

QY 778 TGGTAGTCCCACTTACTCTGGGAGGCTGAGGCAAGAAAATGCTTGAACCCAGAGGCGGA 837
DB 10081 CTATTAATCCCACTTACTCTGGGAGGCTGAGGCAAGAAAATGCTTGAACCCAGAGGCGGA 10022

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QY 838 CGTTGGCGGTAGCGAGATGCGCGCGCTGATTCCAGCGCTGGCGACAAGATGAGACTCC 897
DB 10021 GGTTCAGTAGTGAATGAGATCAAGCCACTGCACTCCAGCTGGGTGAGAGTCAAGTCTT 9962

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

RESULT 14
US-09-949-016-16758/c
; Sequence 16758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16758
; LENGTH: 35678
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16758

Query Match      23.1%; Score 209.2; DB 4; Length 35678;
Best Local Similarity 79.7%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 598 ATTAGCAATTAAACTGAGAAATGGCGCGGCGGCGCTGATCCAGCTGTAATCCCGACA 657
DB 10261 ATATGTAATTAAATAATATAGAGACGCTGGCACAGTGCTTATGCTTATATATCCACGA 10202

QY 658 CTTTGGAGGCGCGAGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCTGGCCA 717
DB 10201 CTTTGGAGGCGCGAGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCTGGCCA 10142

QY 718 ACATGGTGAACCTTGTCTACTAATAAAATTAACCAAGGCAAGTGTGTGCAC 777
DB 10141 ACATGGTGAACCTTGTCTACTAATAAAATTAACCAAGGCAAGTGTGTGCAC 10082

QY 778 TGGTAGTCCCACTTACTCTGGGAGGCTGAGGCAAGAAAATGCTTGAACCCAGAGGCGGA 837
DB 10081 CTATTAATCCCACTTACTCTGGGAGGCTGAGGCAAGAAAATGCTTGAACCCAGAGGCGGA 10022

QY 838 CGTTGGCGGTAGCGAGATGCGCGCGCTGATTCCAGCGCTGGCGACAAGATGAGACTCC 897
DB 10021 GGTTCAGTAGTGAATGAGATCAAGCCACTGCACTCCAGCTGGGTGAGAGTCAAGTCTT 9962

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

RESULT 15
US-09-949-016-16755/c
; Sequence 16755, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 16755
; LENGTH: 58361
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16755

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```

Query Match      23.1%; Score 209.2; DB 4; Length 58361;
Best Local Similarity 79.7%; Pred. No. 5.2e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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QY 598 ATTAGCAATTAAACGTGAGAAATGGGCCGGGCGACGGGTGCTCAGGCTGTATCCGAGCA 657
Db 32944 ATATGTATTAAATAATATAGAGACAGCTGGGCAAGTGGCTTATATATCCAGCA 32885
QY 658 CTTTGGAGGCGCGAGCGGGTGATCAGCTGAGATCAGAGTTCAAGACCAAGCTGGCCA 717
Db 32884 CTTTGGAGGCGCGAGCGGGTGATCAGCTGAGATCAGAGTTCAAGACCAAGCTGGCCA 32825
QY 718 ACATGGTGAAACCTTGTCTACTTAAATAATCAAAAAATTAGCCAGGCAAGTGTGTGCAC 777
Db 32824 ACATGGTGAAACCTTGTCTACTTAAATAATCAAAAAATTAGCTGGGCGGTGTGGCATGCAC 32765
QY 778 TGGTAGTCCCAAGTTACTCGGGAGGCTGAGGCAAGAAATGCTGAACCAAGAGGCGGA 837
Db 32764 CTATTAATCCAGCTACTCGGAGGCTGAGGCAAGAAATGCTGAACCAAGAGGCTGGA 32705
QY 838 CGTTGCGTGAGCGAGATCGCGCCGCTGATTCAGGCTGGGCGACAGAGTGAAGTCC 897
Db 32704 GGTTCAGTGAGTCGAGATCAGCCCACTGCATCCAGCTGGGTGACAGAGTCAAGTCT 32645
QY 898 ATCTCACACA 907
Db 32644 GTCTCAAAAA 32635

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Search completed: September 15, 2005, 18:28:34
Job time : 327 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 15:56:28 ; Search time 3740 Seconds
(without alignment)
9231.094 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 907

Sequence: 1 ggaactcgaagtcacacg.....gtgagactcaccatcacaca 907

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_hic:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	470	51.8	470	2	BF914480 IL3-UT011
C 3	470	51.8	470	2	BF915910 IL3-UT011
C 4	469	51.7	470	2	BF912836 IL3-UT011
C 5	466.4	51.4	792	6	CB985553 AGENCOURT
C 6	458	50.5	480	1	AA464988 z280a06.r
C 7	403	44.4	425	1	AA293138 z26e06.r
C 8	369	40.7	402	1	AA399124 zc49a02.r
C 9	344.2	37.9	360	1	AA481356 zV44d03.r
C 10	334.4	36.9	547	4	BM854082 K-EST0135
C 11	308	34.0	511	4	BF963567 PM1-NN120
C 12	308	34.0	511	4	BI034628 PM1-NN120
C 13	304.8	33.6	308	7	CN277578 17006001
C 14	281.4	31.0	363	1	AL133867 DKFZP761H
C 15	271.2	29.9	319	2	BF903767 PM1-MT019
C 16	238.2	26.3	406	1	AV710673 AV710673
C 17	233.4	25.7	510	4	BC995746 M22-HT116
C 18	231.6	25.5	287	4	BF959092 PM1-NN120
C 19	228.8	25.2	962	2	BF693667 602081854
C 20	222	24.5	1086	4	BM544700 AGENCOURT
C 21	215	23.7	231	2	BF912829 IL3-UT011
C 22	212	23.4	609	6	CB370005 TGESTY96
C 23	211.2	23.3	480	5	BX483243 DKFZP686G
C 24	210.8	23.2	592	5	BP320355 BP320355

C 25	209.2	23.1	481	6	CA391442
C 26	208.6	23.0	640	8	AZ519506
C 27	208.4	23.0	692	1	AV700758
C 28	208.2	23.0	413	1	AV764406
C 29	207.8	22.9	490	7	H59651
C 30	207.8	22.9	521	8	AQ784619 HS_3248-A
C 31	207.4	22.9	398	5	BX484839 DKFZP686K
C 32	207.2	22.8	313	1	AA829665
C 33	207.2	22.8	571	4	BI254712
C 34	206.8	22.8	692	9	AG126921
C 35	206.4	22.8	645	9	AG064993 Pan tregl
C 36	206.2	22.7	583	5	BK494015 DKFZP781J
C 37	205.8	22.7	274	4	BF957905 PM1-NN120
C 38	205.8	22.7	558	4	BM66389 UI-R-COI-
C 39	205.8	22.7	584	5	BP301691
C 40	205	22.6	488	1	AA720582
C 41	205	22.6	745	8	AQ752732
C 42	205	22.6	1500	3	BC021103
C 43	204.6	22.6	514	8	BS1474
C 44	204.6	22.6	810	4	BP688874
C 45	204.4	22.5	429	7	CN264016
C 46	204.4	22.5	487	7	CN275741
C 47	204.4	22.5	686	4	BC819887
C 48	204.4	22.5	687	3	BC019875
C 49	204	22.5	402	5	BO631269
C 50	204	22.5	472	5	BU790005
C 51	204	22.5	472	8	AQ310879
C 52	204	22.5	555	8	AQ316808
C 53	204	22.5	690	9	AG088570
C 54	203.8	22.5	392	5	BQ271642
C 55	203.8	22.5	399	7	W02419
C 56	203.8	22.5	429	2	BS501570
C 57	203.8	22.5	877	2	BQ949414
C 58	203.6	22.4	468	1	AL603499
C 59	203.6	22.4	868	5	BU102171
C 60	203.6	22.4	984	5	BO707135
C 61	203.6	22.4	4374	3	CR749501
C 62	203.2	22.4	643	9	AG129001
C 63	203.2	22.4	670	4	BM671184
C 64	203	22.4	321	2	AW511569
C 65	203	22.4	468	9	AG181502
C 66	202.8	22.4	446	2	BE140949
C 67	202.8	22.4	823	5	BO438489
C 68	202.8	22.4	823	8	AQ741080
C 69	202.6	22.3	393	7	H58293
C 70	202.6	22.3	440	5	BM992670
C 71	202.6	22.3	534	5	BM283237
C 72	202.6	22.3	687	7	AG123074
C 73	202.6	22.3	719	4	BM679548
C 74	202.6	22.3	817	2	BE747923
C 75	202.6	22.3	973	5	BK436546
C 76	202.6	22.3	3443	3	HSM801859
C 77	202.6	22.3	7004	3	CR749209
C 78	202.4	22.3	556	7	CK822725
C 79	202.2	22.3	447	2	BP901147
C 80	202.2	22.3	498	7	CR542874
C 81	202.2	22.3	586	6	CA406158
C 82	202.2	22.3	636	5	BM971480
C 83	202.2	22.3	693	5	AG170941
C 84	202.2	22.3	701	9	AG170941
C 85	202.2	22.3	799	6	CD655686
C 86	202.2	22.3	924	5	BO710195
C 87	202	22.3	320	5	BU588558
C 88	202	22.3	588	8	AQ373949
C 89	202	22.3	661	9	AG059678
C 90	202	22.3	663	8	AQ37381
C 91	201.8	22.2	455	8	AQ379702
C 92	201.6	22.2	498	8	AQ479619
C 93	201.6	22.2	560	8	AQ479619
C 94	201.6	22.2	649	9	AG064568
C 95	201.6	22.2	1998	3	CR623156
C 96	201.4	22.2	383	1	AI369076
C 97	201.4	22.2	394	7	CN278335

CA391442	cg15c09.y
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AV700758	AV700758
AV764406	AV764406
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BF957905	PM1-NN120
BM66389	UI-R-COI-
BP301691	BP301691
AA720582	nm21b01.8
AQ752732	HS_3568_B
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BS1474	CIT9788K-A-
BP688874	602270846
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BC019875	Homo sapi
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BS501570	ht62d07.x
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AL603499	DKFZP686L
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CR749501	Homo sapi
AG129001	Pan tregl
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AG181502	Pan tregl
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AQ741080	HS_2272.A
H58293	yr20f07.tl
BM992670	UI-H-DPO-
BX283237	BM992670
AG123074	Pan tregl
BM679548	UI-R-B00-
BE747923	601580282
BK436546	BK436546
AL136891	Homo sapi
CR749209	Homo sapi
CK822725	1697a04.y
BF901147	IL2-MT01.7
CR542874	DKFZP459M
CA406158	1002307.H
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AG170941	Pan tregl
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CD655686	AGENCOURT
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BU588558	AGENCOURT
AQ373949	RPCI11-15
AG059678	Pan tregl
AQ375515	RPCI11-15
AQ37381	CIT-HSP-2
AQ479702	RPCI-11-2
AQ479619	RPCI-11-2
AG064568	Pan tregl
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AI369076	gw29h03.x
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C 98	201.4	22.2	652	8	AQ26609	RPCI11-75	171	199.2	22.0	577	8	AQ483173	AQ483173
C 99	201.4	22.2	683	9	AG177245	Pan t10g1	172	199.2	22.0	579	7	CR545097	CR545097
C 100	201.4	22.2	894	8	AG738714	HS 5382_B	173	199.2	22.0	635	7	CN265093	CN265093
C 101	201.2	22.2	368	1	AA623009	np79h05.8	174	199.2	22.0	657	9	AG150142	AG150142
C 102	201.2	22.2	417	1	AV733634	AV733634	175	199.2	22.0	674	7	CN341729	CN341729
C 103	201.2	22.2	420	8	AA036829	CIT-HSP-2	176	199.2	22.0	688	7	CR766437	CR766437
C 104	201.2	22.2	494	8	AQ228611	HS 2009_A	177	199.2	22.0	370	8	AQ263765	AQ263765
C 105	201.2	22.2	533	7	CA2880174	UI-H-EDU-	178	199.2	22.0	559	1	AU158606	AU158606
C 106	201.2	22.2	618	5	CA335336	NISC 1409	179	199.2	22.0	612	5	BU952525	BU952525
C 107	201.2	22.2	680	5	BX114339	EX114339	180	199.2	22.0	617	8	AO197170	AO197170
C 108	201.2	22.2	1548	3	CR594735	Full1-1eng	181	199.2	22.0	649	5	BM991864	BM991864
C 109	201.2	22.2	485	8	BE9763	BE9763 CIT-HSP-202	182	199.2	22.0	724	8	B2612696	B2612696
C 110	201.2	22.2	652	5	BX951325	BM991325 DKE2P453P	183	199.2	22.0	374	1	A1282479	A1282479
C 111	201.2	22.2	750	8	AG081408	Pan t10g1	184	199.2	22.0	432	8	AQ477025	AQ477025
C 112	200.8	22.1	353	7	CN271795	AP101680 AP101690	185	199.8	21.9	392	5	BO637025	BO637025
C 113	200.8	22.1	353	7	CN271795	CN271795 170005999	186	199.8	21.9	769	6	CD370173	CD370173
C 114	200.8	22.1	372	5	BM991270	UI-H-DIO-	187	199.8	21.9	897	8	AO744210	AO744210
C 115	200.8	22.1	723	7	CR789995	DKE2P453P	188	199.8	21.9	921	5	BX370271	BX370271
C 116	200.8	22.1	854	6	CD171905	AGENCOURT	189	199.8	21.9	349	7	T24036	T24036
C 117	200.8	22.1	1126	5	BX333363	BX333363	190	199.6	21.9	354	4	BM662676	BM662676
C 118	200.6	22.1	449	8	AE042511	BE042511 ho23b07.x	191	199.6	21.9	354	2	AM177869	AM177869
C 119	200.6	22.1	485	8	AQ219222	HS_3245_B	192	199.6	21.9	515	2	AM177869	AM177869
C 120	200.6	22.1	503	4	BM510027	1997a04.x	193	199.6	21.9	548	7	CN414083	CN414083
C 121	200.6	22.1	744	8	BZ599872	WHACH93TR	194	199.6	21.9	679	2	BS392753	BS392753
C 122	200.6	22.1	785	5	BU657231	AGENCOURT	195	199.6	21.9	694	6	CA420398	CA420398
C 123	200.6	22.1	799	5	BU854310	AGENCOURT	196	199.4	21.9	324	4	BM671251	BM671251
C 124	200.4	22.1	360	1	AI254267	UI-H-DIO-	197	199.4	21.9	390	7	CN272500	CN272500
C 125	200.4	22.1	507	1	AA601712	no03805.8	198	199.4	21.9	426	7	CN395233	CN395233
C 126	200.4	22.1	687	9	AG135036	Pan t10g1	199	199.4	21.9	914	5	CN267428	CN267428
C 127	200.4	22.1	808	4	BG622731	BG622731 602647510	200	199.4	21.9	664	7	BU170914	BU170914
C 128	200.4	22.1	1750	3	AF119908	AGENCOURT	201	199.4	21.9	922	5	BU501973	BU501973
C 129	200.2	22.1	416	1	AV693536	AV693536	202	199.2	21.9	369	5	BK470473	BK470473
C 130	200.2	22.1	420	2	BE062545	BE062545 CV4-BT025	203	199.2	21.9	404	8	B91764	B91764
C 131	200.2	22.1	421	1	AV691556	AV691556	204	199.2	21.9	453	8	AO176505	AO176505
C 132	200.2	22.1	569	7	CN274765	CN274765 170006000	205	199.2	21.9	493	2	AM328331	AM328331
C 133	200.2	22.1	654	7	CR791150	DKE2P469E	206	199.2	21.9	504	4	BI715158	BI715158
C 134	200.2	22.1	690	4	BF971234	602273252	207	199.2	21.9	510	1	AV756056	AV756056
C 135	200.2	22.1	1034	4	BM806909	AGENCOURT	208	199.2	21.9	562	7	CR818567	CR818567
C 136	200.2	22.1	557	4	BM991139	UI-H-DIO-	209	199.2	21.9	580	5	BP264216	BP264216
C 137	200.2	22.1	586	5	BX951238	BX951238 DKE2P781P	210	199.2	21.9	648	8	AO309277	AO309277
C 138	200.2	22.1	621	9	AG102562	Pan t10g1	211	199.2	21.9	669	5	BU950624	BU950624
C 139	200.2	22.1	665	9	AG045689	Pan t10g1	212	199.2	21.9	670	9	AG164774	AG164774
C 140	199.8	22.0	439	1	AI355559	qt75f05.x	213	199.2	21.9	681	9	AG079336	AG079336
C 141	199.8	22.0	466	8	AO483846	RPCI-11-2	214	199.2	21.9	716	9	AC0002485	AC0002485
C 142	199.8	22.0	564	7	CN413054	170005336	215	199.2	21.9	1238	7	BM455282	BM455282
C 143	199.8	22.0	581	2	AW970987	EST833072	216	199.2	21.8	386	7	CT135158	CT135158
C 144	199.8	22.0	595	8	AO424714	CITBI-El-	217	199.2	21.8	387	8	AO196676	AO196676
C 145	199.8	22.0	730	5	BU616124	UI-H-DFO-	218	199.2	21.8	493	5	BU198009	BU198009
C 146	199.8	22.0	837	5	BX486445	DKE2P686O	219	199.2	21.8	504	9	CI423119	CI423119
C 147	199.8	22.0	840	1	AL706641	UI-H-DFO-	220	199.2	21.8	636	2	BE140955	BE140955
C 148	199.8	22.0	919	3	BC013247	BC013247 Homo sapi	221	199.2	21.8	657	8	AO477136	AO477136
C 149	199.8	22.0	960	6	CD245816	AGENCOURT	222	199.2	21.8	887	5	BM423685	BM423685
C 150	199.6	22.0	357	1	AI031759	AI031759 CW39d11.x	223	199.2	21.8	969	3	CR623410	CR623410
C 151	199.6	22.0	423	8	AO059624	CIT-HSP-2	224	199.2	21.8	420	5	BX281326	BX281326
C 152	199.6	22.0	458	2	AM151247	xs34h04.x	225	199.2	21.8	442	2	AW514844	AW514844
C 153	199.6	22.0	572	8	AO763732	HS 3186_A	226	199.2	21.8	442	5	AX280439	AX280439
C 154	199.6	22.0	680	5	BM985796	UI-H-EDU-	227	199.2	21.8	467	8	AO349390	AO349390
C 155	199.6	22.0	681	5	BM016777	UI-H-DIO-	228	199.2	21.8	475	2	AM008184	AM008184
C 156	199.6	22.0	684	5	BO772479	UI-H-FEO-	229	199.2	21.8	478	7	CN265094	CN265094
C 157	199.6	22.0	736	5	BO000441	UI-H-DFO-	230	199.2	21.8	549	9	CB177313	CB177313
C 158	199.6	22.0	862	4	BG762519	602733970	231	199.2	21.8	551	6	CA440586	CA440586
C 159	199.6	22.0	876	6	CD556766	AGENCOURT	232	199.2	21.8	583	5	BP301697	BP301697
C 160	199.6	22.0	909	4	BG034698	602300050	233	199.2	21.8	590	8	AO537619	AO537619
C 161	199.6	22.0	941	5	BX451504	BX451504	234	199.2	21.8	664	7	CN265061	CN265061
C 162	199.6	22.0	3128	3	CR627380	Homo sapi	235	199.2	21.8	672	5	BU617955	BU617955
C 163	199.6	22.0	3243	3	HSB805448	Homo sapi	236	199.2	21.8	699	5	BM712205	BM712205
C 164	199.4	22.0	321	8	BU958280	AGENCOURT	237	197.6	21.8	350	1	AV743179	AV743179
C 165	199.4	22.0	379	8	AO580711	RPCI-11-4	238	197.6	21.8	453	5	BU726699	BU726699
C 166	199.4	22.0	558	5	BU580548	fn35c05.x	239	197.6	21.8	479	1	AI744963	AI744963
C 167	199.4	22.0	604	5	BM990713	UI-H-DIO-	240	197.6	21.8	662	9	AG011122	AG011122
C 168	199.4	22.0	631	9	AG050042	Pan t10g1	241	197.6	21.8	707	5	BX488461	BX488461
C 169	199.4	22.0	4974	3	HSB804886	Homo sapi	242	197.6	21.8	843	5	BO421400	BO421400
C 170	199.2	22.0	427	1	AI123488	qa01f01.x	243	197.6	21.8	957	5	BO441618	BO441618

C 244	197.6	21.8	993	3	AP318326	Homo sapi	317	196.6	21.7	582	5	BP267287	BP267287
C 245	197.6	21.8	3204	3	HSMB04305		318	196.6	21.7	582	5	BP275852	BP275852
C 246	197.6	21.8	5093	3	HSMB09153		319	196.6	21.7	582	5	BP292016	BP292016
C 247	197.4	21.8	324	1	A1247128	qx52g08.x	320	196.6	21.7	583	5	BP268005	BP268005
C 248	197.4	21.8	330	5	BUS65193	AGENCOURT	C 321	196.6	21.7	596	5	BL484036	BL484036
C 249	197.4	21.8	344	1	A1590404	ts10b03.x	C 322	196.6	21.7	601	1	AL708507	AL708507
C 250	197.4	21.8	401	8	AO669103	HS_5414_A	C 323	196.6	21.7	637	8	BM691791	BM691791
C 251	197.4	21.8	492	5	BQ706631	AGENCOURT	C 324	196.6	21.7	645	7	CN362346	CN362346
C 252	197.4	21.8	541	5	BM993720	UI-H-DHO	C 325	196.6	21.7	652	2	BE177530	BE177530
C 253	197.4	21.8	594	5	BX494380	DKF2P779C	C 326	196.6	21.7	701	7	CF125387	CF125387
C 254	197.4	21.8	613	5	BM990533	UI-H-DHO	C 327	196.6	21.7	777	4	BM918656	BM918656
C 255	197.4	21.8	677	7	CK004046	AGENCOURT	C 328	196.6	21.7	824	8	BZ611785	BZ611785
C 256	197.4	21.8	723	7	AC143729	AG143729	C 329	196.6	21.7	879	5	EQ049398	EQ049398
C 257	197.4	21.8	733	6	CA308850	CA308850	C 330	196.6	21.7	1000	5	BM455492	BM455492
C 258	197.4	21.8	902	2	BF034649	BF034649	C 331	196.6	21.7	1023	4	BM918656	BM918656
C 259	197.4	21.8	906	5	BQ227117	AGENCOURT	C 332	196.6	21.7	1143	5	BM918656	BM918656
C 260	197.4	21.8	949	5	BO950110	AGENCOURT	C 333	196.6	21.7	1359	8	AP101912	AP101912
C 261	197.2	21.7	379	1	AV683406	AV683406	C 334	196.6	21.7	1588	3	CR596829	CR596829
C 262	197.2	21.7	396	4	BM040851	BM040851	C 335	196.6	21.7	1588	3	CR596829	CR596829
C 263	197.2	21.7	412	8	AZ518582	AZ518582	C 336	196.6	21.7	3536	3	CR749620	CR749620
C 264	197.2	21.7	420	1	A1760835	A1760835	C 337	196.6	21.7	3974	3	HSMB05841	HSMB05841
C 265	197.2	21.7	477	1	A1924950	wn26b03.x	C 338	196.6	21.7	4747	3	HSMB08075	HSMB08075
C 266	197.2	21.7	516	8	AO691270	AO691270	C 339	196.6	21.7	368	1	AA224966	AA224966
C 267	197.2	21.7	642	7	CN276686	CN276686	C 340	196.4	21.7	458	2	AW272513	AW272513
C 268	197.2	21.7	644	8	AQ478207	AQ478207	C 341	196.4	21.7	464	8	AO632383	AO632383
C 269	197.2	21.7	751	1	A1188382	A1188382	C 342	196.4	21.7	642	5	BH605896	BH605896
C 270	197.2	21.7	399	4	AG223376	AG223376	C 343	196.4	21.7	1042	8	BM605896	BM605896
C 271	197.2	21.7	417	1	AV697609	AV697609	C 344	196.4	21.7	3744	3	BC018955	BC018955
C 272	197.2	21.7	474	7	CR559874	CR559874	C 345	196.4	21.7	319	5	BUS33187	BUS33187
C 273	197.2	21.7	633	9	AG144698	AG144698	C 346	196.2	21.6	352	2	AA503307	AA503307
C 274	197.2	21.7	745	1	AZ517850	AZ517850	C 347	196.2	21.6	456	1	BR328286	BR328286
C 275	197.2	21.7	741	8	AC2517850	RPCT-11-1	C 348	196.2	21.6	372	2	BR328286	BR328286
C 276	197.2	21.7	755	4	BX090291	BX090291	C 349	196.2	21.6	481	8	AI801563	AI801563
C 277	197.2	21.7	770	5	BI860178	BI860178	C 350	196.2	21.6	493	8	B36003	B36003
C 278	197.2	21.7	826	5	BQ438665	BQ438665	C 351	196.2	21.6	498	1	AU144397	AU144397
C 279	197.2	21.7	866	5	BQ172464	BQ172464	C 352	196.2	21.6	567	5	BP267172	BP267172
C 280	197.2	21.7	884	5	BQ711287	BQ711287	C 353	196.2	21.6	568	2	AM813106	AM813106
C 281	197.2	21.7	893	5	BE070660	BE070660	C 354	196.2	21.6	636	7	CN480509	CN480509
C 282	197.2	21.7	900	2	BE880692	BE880692	C 355	196.2	21.6	722	2	BF383027	BF383027
C 283	197.2	21.7	903	2	BE867712	BE867712	C 356	196.2	21.6	778	6	CG963857	CG963857
C 284	197.2	21.7	975	3	CR627281	CR627281	C 357	196.2	21.6	1383	3	CR623768	CR623768
C 285	197.2	21.7	3775	3	AA774223	AA774223	C 358	196.2	21.6	401	2	AW341882	AW341882
C 286	196.8	21.7	323	1	AA774703	AA774703	C 359	196.2	21.6	451	8	AO394853	AO394853
C 287	196.8	21.7	342	1	AA719543	AA719543	C 360	196.2	21.6	521	2	AM957502	AM957502
C 288	196.8	21.7	390	1	BE062476	BE062476	C 361	196.2	21.6	590	6	CD707806	CD707806
C 289	196.8	21.7	416	2	AO342192	AO342192	C 362	196.2	21.6	663	9	AG015017	AG015017
C 290	196.8	21.7	433	8	BM127488	BM127488	C 363	196.2	21.6	694	9	AG002921	AG002921
C 291	196.8	21.7	439	4	BM127488	BM127488	C 364	196.2	21.6	778	6	CG963857	CG963857
C 292	196.8	21.7	477	1	AI761677	AI761677	C 365	196.2	21.6	861	1	AU120423	AU120423
C 293	196.8	21.7	478	1	AI761677	AI761677	C 366	196.2	21.6	1058	4	HSMB07067	HSMB07067
C 294	196.8	21.7	504	8	AO829636	AO829636	C 367	196.2	21.6	5604	3	AA349710	AA349710
C 295	196.8	21.7	504	5	BX490571	DKF2P686F	C 368	196.2	21.6	356	1	AA650528	AA650528
C 296	196.8	21.7	532	4	BM743761	BM743761	C 369	195.8	21.6	362	1	AA650528	AA650528
C 297	196.8	21.7	572	4	BM743761	BM743761	C 370	195.8	21.6	428	5	BP431044	BP431044
C 298	196.8	21.7	587	8	BZ610289	BZ610289	C 371	195.8	21.6	443	8	AO589677	AO589677
C 299	196.8	21.7	604	7	CK001797	CK001797	C 372	195.8	21.6	512	8	AQ120174	AQ120174
C 300	196.8	21.7	709	8	BUE74938	BUE74938	C 373	195.8	21.6	540	1	AL065031	AL065031
C 301	196.8	21.7	718	5	BUE74938	BUE74938	C 374	195.8	21.6	568	1	AL065031	AL065031
C 302	196.8	21.7	730	8	CR615928	CR615928	C 375	195.8	21.6	628	5	BX486761	BX486761
C 303	196.8	21.7	730	8	CR615928	CR615928	C 376	195.8	21.6	669	5	BM997858	BM997858
C 304	196.8	21.7	730	8	CR615928	CR615928	C 377	195.8	21.6	732	8	AO890095	AO890095
C 305	196.8	21.7	730	8	CR615928	CR615928	C 378	195.8	21.6	863	8	AQ738509	AQ738509
C 306	196.6	21.7	732	4	BM710087	BM710087	C 379	195.8	21.6	884	8	AQ738492	AQ738492
C 307	196.6	21.7	732	4	BM710087	BM710087	C 380	195.8	21.6	892	6	CD481383	CD481383
C 308	196.6	21.7	732	4	BM710087	BM710087	C 381	195.8	21.6	354	6	CD481383	CD481383
C 309	196.6	21.7	732	4	BM710087	BM710087	C 382	195.8	21.6	365	8	AO085904	AO085904
C 310	196.6	21.7	732	4	BM710087	BM710087	C 383	195.6	21.6	375	1	AA657392	AA657392
C 311	196.6	21.7	732	4	BM710087	BM710087	C 384	195.6	21.6	377	1	AA657392	AA657392
C 312	196.6	21.7	732	4	BM710087	BM710087	C 385	195.6	21.6	384	1	AA657392	AA657392
C 313	196.6	21.7	732	4	BM710087	BM710087	C 386	195.6	21.6	392	1	AA484892	AA484892
C 314	196.6	21.7	732	4	BM710087	BM710087	C 387	195.6	21.6	396	1	AI355103	AI355103
C 315	196.6	21.7	732	4	BM710087	BM710087	C 388	195.6	21.6	397	8	AQ214855	AQ214855
C 316	196.6	21.7	732	4	BM710087	BM710087	C 389	195.6	21.6	397	8	AQ214855	AQ214855

C 390	195.6	21.6	441	8	A2521019	C 463	195	21.5	680	9	AG077619	AG077619	Pen	trogl
C 391	195.6	21.6	480	7	CN269107	C 464	195	21.5	682	9	AG181743	AG181743	Pen	trogl
C 392	195.6	21.6	500	8	AQ248325	C 465	195	21.5	705	7	CN278633	CN278633	170006003	
C 393	195.6	21.6	521	5	BU617227	C 466	195	21.5	759	5	BU854207	BU854207	AGENCOURT	
C 394	195.6	21.6	529	8	B92837	C 467	195	21.5	722	1	AU136365	AU136365		
C 395	195.6	21.6	566	8	BU072318	C 468	195	21.5	885	8	AQ739135	AQ739135	HS_5387_B	
C 396	195.6	21.6	573	2	AW974923	C 469	195	21.5	886	8	AQ739494	HS_5387_B		
C 397	195.6	21.6	580	1	AU150583	C 470	195	21.5	910	5	BU850247	AGENCOURT		
C 398	195.6	21.6	580	5	BP336490	C 471	195	21.5	914	5	BU149187	AGENCOURT		
C 399	195.6	21.6	580	5	BU053726	C 472	195	21.5	924	5	BC697612	602660853		
C 400	195.6	21.6	598	5	BU017808	C 473	195	21.5	998	5	EX381716	EX381716		
C 401	195.6	21.6	609	9	AG149236	C 474	195	21.5	1007	8	BZ611150	BZ611150	WHAC165TF	
C 402	195.6	21.6	616	9	BU617236	C 475	195	21.5	1035	5	BQ217751	AF130079		
C 403	195.6	21.6	619	8	BS8514	C 476	195	21.5	1769	3	AF130079	BC025771	Homo	sap1
C 404	195.6	21.6	660	7	CR545328	C 477	195	21.5	1850	3	BC025771	AA666295	ac39a10.8	
C 405	195.6	21.6	684	8	AO632073	C 478	194.8	21.5	340	1	AA666295	AV655282	AV655282	
C 406	195.6	21.6	702	9	AG153097	C 479	194.8	21.5	383	1	AV655282	AV655282	nc75d11.x	
C 407	195.6	21.6	729	7	CN302098	C 480	194.8	21.5	394	1	AI1732690	AA467912	nc75d11.x	
C 408	195.6	21.6	731	1	AI687343	C 481	194.8	21.5	420	1	AA467912	AA467912	ab23E03.8	
C 409	195.6	21.6	791	5	BU943219	C 482	194.8	21.5	434	1	AA467912	AI702018	tg20c12.x	
C 410	195.6	21.6	836	4	BG771122	C 483	194.8	21.5	438	1	AI702018	AO391790	CTBT-E1-	
C 411	195.6	21.6	836	4	CR600792	C 484	194.8	21.5	457	8	AO391790	AL036896	DXFZP6864	
C 412	195.6	21.6	1111	5	EX437747	C 485	194.8	21.5	532	1	AL036896	AO406948	HS_5113_A	
C 413	195.4	21.5	342	5	EX480789	C 486	194.8	21.5	537	8	AO406948	AO406948	HS_5113_A	
C 414	195.4	21.5	352	1	AI701898	C 487	194.8	21.5	553	1	AI158457	AG040162	Pen	trogl
C 415	195.4	21.5	421	1	AI7473671	C 488	194.8	21.5	653	9	AG054232	AG15757	Pen	trogl
C 416	195.4	21.5	427	2	AM880986	C 489	194.8	21.5	658	9	AG15757	AG054232	Pen	trogl
C 417	195.4	21.5	439	8	AO768011	C 490	194.8	21.5	733	8	AG15757	AG15757	Pen	trogl
C 418	195.4	21.5	450	7	TS1920	C 491	194.8	21.5	768	8	AO546618	AO546618	CTBT-E1-	
C 419	195.4	21.5	505	7	EX952682	C 492	194.8	21.5	825	8	BZ601462	BZ601462	WHAA145TR	
C 420	195.4	21.5	510	8	AQ477081	C 493	194.8	21.5	933	8	AO743038	AO743038	HS_5387_B	
C 421	195.4	21.5	510	5	BU590031	C 494	194.8	21.5	1107	5	EX438918	EX438918		
C 422	195.4	21.5	528	7	CN263775	C 495	194.8	21.5	6789	3	HSMB07629	HSMB07629		
C 423	195.4	21.5	528	7	CR818107	C 496	194.6	21.5	398	1	AI798521	AI798521	tr36e12.x	
C 424	195.4	21.5	586	1	AI207422	C 497	194.6	21.5	440	8	AQ027499	AQ027499	CTT-HSP-2	
C 425	195.4	21.5	615	8	AQ345915	C 498	194.6	21.5	449	8	AQ062661	AQ062661	CTT-HSP-2	
C 426	195.4	21.5	714	9	AG122688	C 499	194.6	21.5	457	8	B55517	B55517	CTT-HSP-387	
C 427	195.2	21.5	359	7	F23338	C 500	194.6	21.5	508	8	AQ125893	AQ125893	HS_3033_A	
C 428	195.2	21.5	360	6	CI4614	C 501	194.6	21.5	535	5	AO395337	AO395337	CTBT-E1-	
C 429	195.2	21.5	385	6	CB296760	C 502	194.6	21.5	539	8	AO544113	AO544113	RPCT-11-3	
C 430	195.2	21.5	405	1	AI280535	C 503	194.6	21.5	619	7	CF146583	CF146583	UT-HF-C80	
C 431	195.2	21.5	415	5	EX116453	C 504	194.6	21.5	658	9	AG087949	AG087949	Pen	trogl
C 432	195.2	21.5	437	5	EX489723	C 505	194.6	21.5	664	1	AL120004	AL120004	DXFZP761G	
C 433	195.2	21.5	443	8	AQ434649	C 506	194.6	21.5	669	5	EX951401	EX951401	DXFZP781H	
C 434	195.2	21.5	488	4	BM505317	C 507	194.6	21.5	675	5	BM991716	BM991716	UT-HF-DF1-	
C 435	195.2	21.5	503	1	AA604149	C 508	194.6	21.5	701	9	AG144939	AG144939	Pen	trogl
C 436	195.2	21.5	542	5	BU001553	C 509	194.6	21.5	704	7	CF122920	CF122920	UT-HF-C80	
C 437	195.2	21.5	543	1	AA019919	C 510	194.6	21.5	706	9	AV759354	AV759354		
C 438	195.2	21.5	552	2	AM970588	C 511	194.6	21.5	708	9	AG154962	AG154962	Pen	trogl
C 439	195.2	21.5	602	5	BU657458	C 512	194.6	21.5	712	9	AG095201	AG095201		
C 440	195.2	21.5	633	9	AG094873	C 513	194.6	21.5	877	5	EX457314	EX457314	EX457314	
C 441	195.2	21.5	656	4	BSG98542	C 514	194.6	21.5	1071	5	EX402079	EX402079		
C 442	195.2	21.5	660	9	AG011123	C 515	194.6	21.5	1210	5	CR598366	CR598366	Full-1eng	
C 443	195.2	21.5	681	5	BQ477500	C 516	194.6	21.4	359	8	AQ085420	HS_2270_B		
C 444	195.2	21.5	769	8	AQ015528	C 517	194.4	21.4	366	1	AI283938	qt71e11.x		
C 445	195.2	21.5	794	9	AG090076	C 518	194.4	21.4	392	1	AI311796	GO91E05.x		
C 446	195.2	21.5	951	5	BO710495	C 519	194.4	21.4	402	4	BG221988	BS021988	REST41806	
C 447	195.2	21.5	1758	3	BC004550	C 520	194.4	21.4	412	2	BE062478	BE062478	QV4-ET025	
C 448	195	21.5	353	2	BF805088	C 521	194.4	21.4	427	2	AW272815	AW272815	xu24D06.x	
C 449	195	21.5	393	8	AQ771301	C 522	194.4	21.4	432	8	B31519	B31519	HS-1011-A1-	
C 450	195	21.5	400	1	AI268818	C 523	194.4	21.4	477	8	AQ126239	AQ126239	QV0-EN005	
C 451	195	21.5	447	1	AI281622	C 524	194.4	21.4	512	2	BF846619	BF846619	QV0-EN005	
C 452	195	21.5	459	5	EX481314	C 525	194.4	21.4	523	4	BM504793	BM504793	ig90e09.x	
C 453	195	21.5	468	7	CN348180	C 526	194.4	21.4	526	5	EX475994	EX475994	DXFZP6861	
C 454	195	21.5	488	7	CR824505	C 527	194.4	21.4	604	7	CR822516	CR822516	ig90e09.y	
C 455	195	21.5	527	7	CR554971	C 528	194.4	21.4	635	7	CR629762	DXFZP469F		
C 456	195	21.5	527	8	AQ466047	C 529	194.4	21.4	647	2	AW979158	ESTJ31268		
C 457	195	21.5	530	7	CR544735	C 530	194.4	21.4	672	9	AG066531	Pen	trogl	
C 458	195	21.5	559	7	CN348183	C 531	194.4	21.4	681	9	AG182173	Pen	trogl	
C 459	195	21.5	566	5	BP266899	C 532	194.4	21.4	686	9	AG117862	Pen	trogl	
C 460	195	21.5	624	5	EX509953	C 533	194.4	21.4	688	9	AG182171	Pen	trogl	
C 461	195	21.5	640	7	CF128614	C 534	194.4	21.4	699	9	BG570479	BG570479		
C 462	195	21.5	665	7	CN270895	C 535	194.4	21.4	816	5	BU173801	BU173801	AGENCOURT	

C 536	194.4	21.4	826	5	BQ220083	BQ220083	AGENCOURT	C 609	194	21.4	1613	3	CR591695
537	194.4	21.4	907	5	BQ710503	BQ710503	AGENCOURT	C 610	193.8	21.4	283	4	BI007641
538	194.4	21.4	916	5	BF983617	BF983617	602304735	C 611	193.8	21.4	409	1	AA676592
C 539	194.4	21.4	986	5	BUS01670	BUS01670	AGENCOURT	C 612	193.8	21.4	426	2	AW771062
C 540	194.2	21.4	320	5	BUS87770	BUS87770	AGENCOURT	C 613	193.8	21.4	441	2	BF738059
C 541	194.2	21.4	354	8	AQ277656	AQ277656	CITBI-RI-	C 614	193.8	21.4	469	6	CD691341
C 542	194.2	21.4	368	7	N23099	N23099	YV43906.81	C 615	193.8	21.4	486	6	CA848153
C 543	194.2	21.4	421	8	AQ064654	AQ064654	HS_2210_A	C 616	193.8	21.4	521	8	AQ777326
544	194.2	21.4	433	6	CD237813	CD237813	FNPAPH01	C 617	193.8	21.4	531	8	AQ777326
C 545	194.2	21.4	484	1	AA055647	AA055647	2175d03.8	C 618	193.8	21.4	551	2	AW576914
C 546	194.2	21.4	485	8	AQ139069	AQ139069	HS_3082_B	C 619	193.8	21.4	616	6	CB067437
C 547	194.2	21.4	522	8	AQ155894	AQ155894	HS_3197_B	C 620	193.8	21.4	629	9	AG092046
C 548	194.2	21.4	529	5	BQ637931	BQ637931	hdi16d01.y	C 621	193.8	21.4	630	7	CA430112
C 549	194.2	21.4	533	5	AU151751	AU151751	AU151751	C 622	193.8	21.4	632	6	CA310364
C 550	194.2	21.4	560	1	AU147849	AU147849	AU147849	C 623	193.8	21.4	646	8	AQ313437
C 551	194.2	21.4	573	1	BE143664	BE143664	MRO-HT016	C 624	193.8	21.4	656	4	BG547155
C 552	194.2	21.4	579	2	BE143664	BE143664	MRO-HT016	C 625	193.8	21.4	665	5	AG041398
C 553	194.2	21.4	608	1	AL1706835	AL1706835	UI-H-D10-	C 626	193.8	21.4	666	5	BX504233
C 554	194.2	21.4	626	5	BQ016577	BQ016577	UI-H-D10-	C 627	193.8	21.4	704	9	AG117725
C 555	194.2	21.4	634	5	BX480648	BX480648	DKF2p686J	C 628	193.8	21.4	733	5	BX645097
C 556	194.2	21.4	690	9	AG185250	AG185250	Pan t1091	C 629	193.8	21.4	829	8	AF102038
C 557	194.2	21.4	694	7	CF124970	CF124970	UI-HF-EL0	C 630	193.8	21.4	1053	4	BF970033
C 558	194.2	21.4	698	7	BO183396	BO183396	UI-H-ET0-	C 631	193.8	21.4	1064	5	BM906989
C 559	194.2	21.4	707	6	CA439571	CA439571	UI-H-ET0-	C 632	193.8	21.4	1077	1	AL524675
C 560	194.2	21.4	716	7	AF101676	AF101676	AF101676	C 633	193.8	21.4	1102	7	AL569764
C 561	194.2	21.4	721	8	AF101676	AF101676	WHABT33TF	C 634	193.8	21.4	1325	7	F00688
C 562	194.2	21.4	749	8	BZ606363	BZ606363	MR3-HN006	C 635	193.6	21.3	325	5	BX105637
C 563	194.2	21.4	857	5	BUI899543	BUI899543	AGENCOURT	C 636	193.6	21.3	359	5	AX124663
C 564	194.2	21.4	868	6	CD518645	CD518645	AGENCOURT	C 637	193.6	21.3	400	8	AQ124663
C 565	194.2	21.4	919	4	BP967724	BP967724	602287586	C 638	193.6	21.3	409	1	AI287380
C 566	194.2	21.4	934	5	BQ708108	BQ708108	AGENCOURT	C 639	193.6	21.3	427	8	AQ473288
C 567	194.2	21.4	3250	3	BSM804841	BSM804841	Homo bap1	C 640	193.6	21.3	439	7	F45056
C 568	194	21.4	325	9	ACG66257	ACG66257	Homo bap1	C 641	193.6	21.3	506	4	BI439760
C 569	194	21.4	326	9	ACG66257	ACG66257	Homo bap1	C 642	193.6	21.3	506	8	AQ283914
C 570	194	21.4	343	2	BF445745	BF445745	AG189419	C 643	193.6	21.3	520	7	CN273753
C 571	194	21.4	403	1	AQ125355	AQ125355	HS_2168_A	C 644	193.6	21.3	535	1	AU158095
C 572	194	21.4	413	8	AV761486	AV761486	AV761486	C 645	193.6	21.3	543	5	BU677401
C 573	194	21.4	427	8	AQ564751	AQ564751	n160h10.8	C 646	193.6	21.3	585	9	BM045436
C 574	194	21.4	469	1	AA526542	AA526542	n160h10.8	C 647	193.6	21.3	639	9	AG019704
C 575	194	21.4	474	8	AQ474083	AQ474083	CITBI-RI-	C 648	193.6	21.3	661	9	AG033142
C 576	194	21.4	482	8	AQ474083	AQ474083	CITBI-RI-	C 649	193.6	21.3	678	7	CR629996
C 577	194	21.4	482	8	AQ474083	AQ474083	CITBI-RI-	C 650	193.6	21.3	678	8	AQ648411
C 578	194	21.4	490	2	BE142845	BE142845	MRO-HT015	C 651	193.6	21.3	680	8	AQ648411
C 579	194	21.4	504	8	AQ727006	AQ727006	HS_5431_A	C 652	193.6	21.3	691	1	AV699555
C 580	194	21.4	508	2	AW819483	AW819483	RC5-ST029	C 653	193.6	21.3	692	8	AQ780023
C 581	194	21.4	515	1	AI1860648	AI1860648	w104c07.x	C 654	193.6	21.3	762	8	AQ311398
C 582	194	21.4	544	1	AU148232	AU148232	UI-H-EU0-	C 655	193.6	21.3	763	6	CB310811
C 583	194	21.4	566	2	AM966643	AM966643	EST378717	C 656	193.6	21.3	856	8	AQ750055
C 584	194	21.4	574	7	BP220813	BP220813	BP220813	C 657	193.6	21.3	903	4	BG120824
C 585	194	21.4	580	5	CD686671	CD686671	EST3192.h	C 658	193.6	21.3	920	5	BU957399
C 586	194	21.4	582	6	BP355272	BP355272	BP355272	C 659	193.6	21.3	1112	5	BU957399
C 587	194	21.4	583	5	BP217403	BP217403	BP217403	C 660	193.4	21.3	388	8	AQ125136
C 588	194	21.4	583	5	BP217403	BP217403	BP217403	C 661	193.4	21.3	413	1	AI7661120
C 589	194	21.4	588	1	AU146999	AU146999	FLC5087.H	C 662	193.4	21.3	419	2	AW243817
C 590	194	21.4	595	1	AI144575	AI144575	FLC5087.H	C 663	193.4	21.3	450	8	AO615941
C 591	194	21.4	613	2	AW844636	AW844636	RC3-CN005	C 664	193.4	21.3	453	1	AI732682
C 592	194	21.4	651	3	BX478977	BX478977	DKF2p686F	C 665	193.4	21.3	522	5	BX494125
C 593	194	21.4	675	4	BM679573	BM679573	UI-E-E00-	C 666	193.4	21.3	523	8	AQ387570
C 594	194	21.4	698	9	AG108821	AG108821	Pan t1091	C 667	193.4	21.3	562	5	BQ086285
C 595	194	21.4	700	9	AG163691	AG163691	Pan t1091	C 668	193.4	21.3	570	7	CR542889
C 596	194	21.4	701	9	AG015221	AG015221	Homo bap1	C 669	193.4	21.3	571	7	CR822946
C 597	194	21.4	707	9	AG175061	AG175061	Pan t1091	C 670	193.4	21.3	589	8	AQ535498
C 598	194	21.4	726	6	BU627512	BU627512	UI-H-FG0-	C 671	193.4	21.3	620	9	AG154733
C 599	194	21.4	731	6	CD239228	CD239228	FNPMA10	C 672	193.4	21.3	625	6	CB154550
C 600	194	21.4	742	6	BE890203	BE890203	601513183	C 673	193.4	21.3	636	7	CR772671
C 601	194	21.4	750	2	BX643228	BX643228	DKF2p781F	C 674	193.4	21.3	640	9	AG014547
C 602	194	21.4	760	5	BM905333	BM905333	AGENCOURT	C 675	193.4	21.3	649	5	BQ775313
C 603	194	21.4	775	5	BQ009047	BQ009047	UI-H-E10-	C 676	193.4	21.3	669	9	AG060838
C 604	194	21.4	800	1	AU140619	AU140619	AGENCOURT	C 677	193.4	21.3	678	9	AG090115
C 605	194	21.4	824	8	BZ601516	BZ601516	WHABF38TR	C 678	193.4	21.3	685	8	BZ610285
C 606	194	21.4	824	8	BM453994	BM453994	AGENCOURT	C 679	193.4	21.3	688	2	BF792103
C 607	194	21.4	899	4	CR599858	CR599858	full1-Jeng	C 680	193.4	21.3	2144	3	AF130089
C 608	194	21.4	1580	3	CR599858	CR599858	full1-Jeng	C 681	193.4	21.3	2144	3	AF130089

682	193.4	21.3	2856	3	HS80803730	AL832422 Homo sapi	C 755	192.8	21.3	523	8	A2517953	A2517953 RPT-11-3
C 683	193.4	21.3	3205	5	CR749792	CR749792 Homo sapi	C 756	192.8	21.3	532	5	BU947715	BU947715 i05602.x
C 684	193.2	21.3	3501	5	BUS36659	BUS36659 AGENCOURT	C 757	192.8	21.3	570	1	AUI45239	AUI45239 AUI45239
C 685	193.2	21.3	347	1	AA809546	AA809546 nj43c09.b	C 758	192.8	21.3	584	1	AQ473656	AQ473656 CITBI-E1-
C 686	193.2	21.3	377	5	BU960486	BU960486 AGENCOURT	C 759	192.8	21.3	599	1	A1636422	A1636422 tz79c01.x
C 687	193.2	21.3	418	1	AA148618	AA148618 z009c07.b	C 760	192.8	21.3	605	8	AQ347764	AQ347764 RPT-11-13
C 688	193.2	21.3	452	1	A1446623	A1446623 tj25d05.x	C 761	192.8	21.3	609	1	AV702857	AV702857 AV702857
C 689	193.2	21.3	485	2	BF830052	BF830052 MR3-HN005	C 762	192.8	21.3	612	7	CK905828	CK905828 i187e03.x
C 690	193.2	21.3	488	1	AA568127	AA568127 nf13dl2.b	C 763	192.8	21.3	616	7	CK905828	CK905828 i187e03.x
C 691	193.2	21.3	498	8	AQ285474	AQ285474 RPT-11-78	C 764	192.8	21.3	617	8	BI6477	BI6477 B16477
C 692	193.2	21.3	512	5	BK642749	BK642749 DKE2P781G	C 765	192.8	21.3	651	9	AG037309	AG037309 Pan troy1
C 693	193.2	21.3	550	6	CD687373	CD687373 EST3894.h	C 766	192.8	21.3	658	7	CK430849	CK430849 OJ54f11.y
C 694	193.2	21.3	560	1	AL602775	AL602775 DKE2P6861	C 767	192.8	21.3	669	8	AQ353815	AQ353815 RPT-11-10
C 695	193.2	21.3	577	1	AV732057	AV732057 AV732057	C 768	192.8	21.3	746	5	BE632972	BE632972 UI-H-DP0-
C 696	193.2	21.3	579	8	AQ546539	AQ546539 CITBI-E1-	C 769	192.8	21.3	1007	1	AL544410	AL544410 AL544410
C 697	193.2	21.3	589	2	AM162555	AM162555 au77d06.x	C 770	192.8	21.3	1176	3	CR612626	CR612626 full-leng
C 698	193.2	21.3	594	5	BQ272418	BQ272418 i198g01.x	C 771	192.6	21.2	346	5	BM991496	BM991496 UI-H-DH0-
C 699	193.2	21.3	604	8	A2517781	A2517781 RPT-11-1	C 772	192.6	21.2	370	5	BQ711408	BQ711408 AGENCOURT
C 700	193.2	21.3	638	4	BG427437	BG427437 602499161	C 773	192.6	21.2	420	1	A1049999	A1049999 an22a12.x
C 701	193.2	21.3	647	5	BK502809	BK502809 DKE2P779C	C 774	192.6	21.2	519	8	AQ358500	AQ358500 RPT-11-3
C 702	193.2	21.3	658	7	H80463	H80463 y075D05.r1	C 775	192.6	21.2	546	5	BU899282	BU899282 AGENCOURT
C 703	193.2	21.3	661	1	AV730440	AV730440 AV730440	C 776	192.6	21.2	579	1	AUI44608	AUI44608 AUI44608
C 704	193.2	21.3	681	9	AG015022	AG015022 Homo sapi	C 777	192.6	21.2	582	5	BP250579	BP250579 BP250579
C 705	193.2	21.3	714	6	CD366358	CD366358 UI-H-FT1-	C 778	192.6	21.2	628	6	CA306131	CA306131 UI-H-FT1-
C 706	193.2	21.3	767	1	AV700498	AV700498 AV700498	C 779	192.6	21.2	639	8	AQ018913	AQ018913 CIT-HSP-2
C 707	193.2	21.3	781	8	BZ71947	BZ71947 mce82h06.f	C 780	192.6	21.2	655	9	AG080004	AG080004 Pan troy1
C 708	193.2	21.3	799	8	BZ610948	BZ610948 WHADL64TF	C 781	192.6	21.2	656	9	AG035209	AG035209 Pan troy1
C 709	193.2	21.3	888	5	BU162525	BU162525 AGENCOURT	C 782	192.6	21.2	658	8	AQ393450	AQ393450 CITBI-E1-
C 710	193.2	21.3	900	5	BU957335	BU957335 AGENCOURT	C 783	192.6	21.2	668	7	CK003906	CK003906 AGENCOURT
C 711	193.2	21.3	917	5	BU963586	BU963586 AGENCOURT	C 784	192.6	21.2	688	5	BQ652218	BQ652218 AGENCOURT
C 712	193.2	21.3	2110	3	BC012538	BC012538 Homo sapi	C 785	192.6	21.2	695	5	BU629128	BU629128 UI-H-PL0-
C 713	193.2	21.3	298	1	AA228979	AA228979 nc50a06.x	C 786	192.6	21.2	698	6	CA306826	CA306826 UI-H-FT1-
C 714	193.2	21.3	311	5	BU603673	BU603673 AGENCOURT	C 787	192.6	21.2	716	5	BM969125	BM969125 UI-CF-ENO
C 715	193.2	21.3	324	2	AM0985626	AM0985626 xh41e01.x	C 788	192.6	21.2	718	2	BE883957	BE883957 601505473
C 716	193.2	21.3	354	7	NE5456	NE5456 y48e04.b1	C 789	192.6	21.2	756	5	EX341284	EX341284 EX341284
C 717	193.2	21.3	363	1	AA704393	AA704393 z186h04.b	C 790	192.6	21.2	803	6	CB962282	CB962282 AGENCOURT
C 718	193.2	21.3	374	4	BI492613	BI492613 dE26g09.w	C 791	192.6	21.2	901	5	BQ230657	BQ230657 AGENCOURT
C 719	193.2	21.3	375	2	AM021674	AM021674 dE26g09.y	C 792	192.6	21.2	941	6	CD518779	CD518779 AGENCOURT
C 720	193.2	21.3	382	1	AA568433	AA568433 nf16f09.b	C 793	192.6	21.2	968	2	BF345228	BF345228 602018175
C 721	193.2	21.3	388	8	AQ212798	AQ212798 HS_3118.B	C 794	192.6	21.2	1055	5	BQ948298	BQ948298 AGENCOURT
C 722	193.2	21.3	413	8	AQ664805	AQ664805 HS_5303.B	C 795	192.6	21.2	1113	5	EX444493	EX444493 EX444493
C 723	193.2	21.3	433	8	AM157128	AM157128 au82g09.x	C 796	192.6	21.2	1130	3	HS860069	HS860069
C 724	193.2	21.3	441	8	B80074	B80074 CIT-HSP-204	C 797	192.6	21.2	3341	3	CR749847	CR749847 Homo sapi
C 725	193.2	21.3	456	2	AM897556	AM897556 CM3-NN005	C 798	192.6	21.2	3637	3	BC038671	BC038671 Homo sapi
C 726	193.2	21.3	464	7	CS383117	CS383117 DKE2P459L	C 799	192.4	21.2	291	2	AW242234	AW242234 x024a05.x
C 727	193.2	21.3	480	6	CD679321	CD679321 hq08f05.y	C 800	192.4	21.2	302	4	BG966738	BG966738 CM0-HRT129
C 728	193.2	21.3	536	8	AQ393821	AQ393821 CITBI-E1-	C 801	192.4	21.2	353	1	AA332320	AA332320 EST26067
C 729	193.2	21.3	541	1	AUI44497	AUI44497 AUI44497	C 802	192.4	21.2	356	8	AQ817094	AQ817094 HS_5553.A
C 730	193.2	21.3	552	7	CM264709	CM264709 170004244	C 803	192.4	21.2	366	1	A1911605	A1911605 wC86b01.x
C 731	193.2	21.3	553	5	BK484034	BK484034 DKE2P686A	C 804	192.4	21.2	379	1	A1290008	A1290008 qW25g10.x
C 732	193.2	21.3	561	8	AQ387133	AQ387133 RPT-11-14	C 805	192.4	21.2	387	6	CD708587	CD708587 EST25114
C 733	193.2	21.3	564	4	BI467196	BI467196 iC19c04.x	C 806	192.4	21.2	393	3	B87031	B87031 RPT-11-27B1
C 734	193.2	21.3	583	1	AL600288	AL600288 DKE2P313A	C 807	192.4	21.2	402	8	AO527301	AO527301 CITBI-E1-
C 735	193.2	21.3	619	7	CN414232	CN414232 170005830	C 808	192.4	21.2	406	8	B91247	B91247 CIT-HSP-216
C 736	193.2	21.3	642	8	B59854	B59854 CIT-HSP-345	C 809	192.4	21.2	407	1	AA122196	AA122196 ae73b04.8
C 737	193.2	21.3	629	8	AQ473496	AQ473496 CITBI-E1-	C 810	192.4	21.2	435	1	AA122175	AA122175 zn29a05.8
C 738	193.2	21.3	648	8	BZ611349	BZ611349 WHAAO01TR	C 811	192.4	21.2	441	1	A1674873	A1674873 wC77f09.x
C 739	193.2	21.3	663	4	BM742716	BM742716 K-EST0015	C 812	192.4	21.2	447	8	AQ484712	AQ484712 RPT-11-2
C 740	193.2	21.3	681	8	BZ772377	BZ772377 mcv35909.f	C 813	192.4	21.2	467	4	BI438872	BI438872 iC27g01.x
C 741	193.2	21.3	698	9	AG119007	AG119007 Pan troy1	C 814	192.4	21.2	477	7	CR738128	CR738128 CR738128
C 742	193.2	21.3	721	7	CR790056	CR790056 DKE2P459G	C 815	192.4	21.2	483	3	BP913232	BP913232 I13-DT011
C 743	193.2	21.3	809	7	CK232499	CK232499 ILLUMIGEN	C 816	192.4	21.2	490	2	BE138757	BE138757 xW94f09.x
C 744	193.2	21.3	839	5	BK400315	BK400315 BX400315	C 817	192.4	21.2	498	5	BM959211	BM959211 UI-H-ED0-
C 745	193.2	21.3	874	5	CR599555	CR599555 full-leng	C 818	192.4	21.2	504	8	BZ605467	BZ605467 WHABM65TF
C 746	193.2	21.3	1890	3	BC048794	BC048794 Homo sapi	C 819	192.4	21.2	507	1	AA313025	AA313025 EST138843
C 747	193.2	21.3	2493	3	BC048794	BC048794 Homo sapi	C 820	192.4	21.2	518	4	BM090960	BM090960 iS18d05.x
C 748	192.8	21.3	346	1	AA084148	AA084148 zn17c03.8	C 821	192.4	21.2	545	8	AQ268517	AQ268517 RPT-11-76
C 749	192.8	21.3	371	7	CK000820	CK000820 AGENCOURT	C 822	192.4	21.2	561	4	BI438652	BI438652 iC25a09.x
C 750	192.8	21.3	425	2	AM513569	AM513569 x086f03.x	C 823	192.4	21.2	566	1	AL597545	AL597545 DKE2P313H
C 751	192.8	21.3	430	2	AM513556	AM513556 x086f03.x	C 824	192.4	21.2	569	6	CA943760	CA943760 i184f10.x
C 752	192.8	21.3	493	8	BH912810	BH912810 UP_354-9K	C 825	192.4	21.2	570	1	AUI49443	AUI49443 AUI49443
C 753	192.8	21.3	507	5	BQ787605	BQ787605 i1m13b03.x	C 826	192.4	21.2	571	8	AQ381323	AQ381323 RPT-11-13
C 754	192.8	21.3	512	2	AM473541	AM473541 hb05f03.x	C 827	192.4	21.2	580	7	CK904663	CK904663 i685f09.y

C 828	192.4	21.2	585	1	AT571894	901	192.2	21.2	716	9	AG185992
829	192.4	21.2	606	5	BQ778458	902	192.2	21.2	733	6	CA429976
830	192.4	21.2	607	5	BX508704	903	192.2	21.2	734	6	CA415430
C 831	192.4	21.2	617	5	BO632031	C 904	192.2	21.2	751	7	CN409704
832	192.4	21.2	618	7	CN264754	905	192.2	21.2	775	5	BX351849
C 833	192.4	21.2	619	5	BX505458	906	192.2	21.2	783	8	AO353737
C 834	192.4	21.2	621	5	BQ883717	907	192.2	21.2	787	5	BM999347
C 835	192.4	21.2	621	7	CN263879	C 908	192.2	21.2	807	5	BU930326
C 836	192.4	21.2	632	7	BQ045015	C 909	192.2	21.2	904	5	BU168982
837	192.4	21.2	652	1	AG087320	C 910	192.2	21.2	1034	3	BU188260
C 838	192.4	21.2	654	1	AU117926	C 911	192.2	21.2	1864	3	CR613024
C 839	192.4	21.2	656	6	CA420015	C 912	192.2	21.2	1884	3	CR594104
840	192.4	21.2	665	7	CN277676	C 913	192.2	21.2	1886	3	CR625365
841	192.4	21.2	668	9	AG169531	C 914	192.2	21.2	1909	3	CR597717
842	192.4	21.2	684	4	BG333118	C 915	192.2	21.2	1916	3	CR622212
843	192.4	21.2	709	6	CD237100	C 916	192.2	21.2	2442	3	CR618116
C 844	192.4	21.2	712	6	CD346087	C 917	192.2	21.2	309	1	AA847341
C 845	192.4	21.2	721	6	CD364665	C 918	192	21.2	343	1	AA636077
C 846	192.4	21.2	722	7	CN263776	C 919	192	21.2	346	6	CD357102
C 847	192.4	21.2	737	5	BX504515	C 920	192	21.2	346	5	BU929075
C 848	192.4	21.2	745	9	AG085464	C 921	192	21.2	353	5	BU929075
C 849	192.4	21.2	754	8	BZ605835	C 922	192	21.2	354	1	AW176687
C 850	192.4	21.2	778	6	CB985162	C 923	192	21.2	354	2	AW182182
851	192.4	21.2	779	6	CA442904	C 924	192	21.2	375	2	AW182182
852	192.4	21.2	795	7	CF595558	C 925	192	21.2	381	2	BE045167
853	192.4	21.2	885	6	CD514239	C 926	192	21.2	447	6	CA434025
854	192.4	21.2	888	7	CF456538	C 927	192	21.2	447	8	B36431
855	192.4	21.2	1104	5	BX358486	C 928	192	21.2	449	8	AO058688
C 856	192.4	21.2	1486	3	CR623651	C 929	192	21.2	477	8	AO198159
C 857	192.4	21.2	3540	3	CR749327	C 930	192	21.2	490	6	CA439033
C 858	192.4	21.2	361	1	AA661583	C 931	192	21.2	526	7	CR556759
C 859	192.2	21.2	377	1	AI452836	C 932	192	21.2	532	4	BP944736
C 860	192.2	21.2	406	8	AO213918	C 933	192	21.2	533	7	T76991
861	192.2	21.2	418	8	AO427676	C 934	192	21.2	538	8	AO417891
C 862	192.2	21.2	420	8	BE005811	C 935	192	21.2	542	6	CD691103
C 863	192.2	21.2	445	1	AI497824	C 936	192	21.2	546	1	AI889995
C 864	192.2	21.2	457	8	AO224277	C 937	192	21.2	546	8	BZ603328
C 865	192.2	21.2	468	5	BX101540	C 938	192	21.2	550	5	BU568083
C 866	192.2	21.2	474	2	BE089811	C 939	192	21.2	554	1	AL713338
867	192.2	21.2	483	1	AA975779	C 940	192	21.2	568	2	BE144554
C 868	192.2	21.2	484	8	AO553388	C 941	192	21.2	580	4	BG830620
C 869	192.2	21.2	493	8	BE545742	C 942	192	21.2	598	2	BE147603
C 870	192.2	21.2	499	8	AO353985	C 943	192	21.2	614	2	AW151824
C 871	192.2	21.2	517	8	AO346199	C 944	192	21.2	620	1	AV719906
C 872	192.2	21.2	518	1	AI573198	C 945	192	21.2	620	2	AM960129
C 873	192.2	21.2	526	6	CA439937	C 946	192	21.2	623	8	AO355723
C 874	192.2	21.2	534	5	BX502385	C 947	192	21.2	623	8	AO550760
C 875	192.2	21.2	564	8	AO006837	C 948	192	21.2	665	5	BM991115
C 876	192.2	21.2	569	4	BM263248	C 949	192	21.2	685	9	AG176669
C 877	192.2	21.2	569	4	BM353667	C 950	192	21.2	698	9	CD239400
C 878	192.2	21.2	577	8	AO483308	C 951	192	21.2	733	7	CR742950
C 879	192.2	21.2	584	5	BP205616	C 952	192	21.2	747	7	BC547968
C 880	192.2	21.2	591	6	CB055261	C 953	192	21.2	801	4	BC032901
C 881	192.2	21.2	598	2	BE276686	C 954	192	21.2	874	3	BX430934
C 882	192.2	21.2	604	4	BM740671	C 955	192	21.2	894	5	BX430935
C 883	192.2	21.2	606	6	CA423390	C 956	192	21.2	932	5	BO959144
884	192.2	21.2	609	8	AO540554	C 957	192	21.2	933	5	BO959144
C 885	192.2	21.2	612	7	CR818280	C 958	192	21.2	970	4	BG118544
C 886	192.2	21.2	629	7	CN360036	C 959	192	21.2	1054	3	CR605219
C 887	192.2	21.2	630	2	AM957739	C 960	192	21.2	1247	3	CR605219
C 888	192.2	21.2	636	8	AO266645	C 961	192	21.2	1616	3	CR613023
C 889	192.2	21.2	660	5	BX642324	C 962	192	21.2	2352	3	CR620185
C 890	192.2	21.2	683	5	BU184851	C 963	191.8	21.1	330	1	AA503142
C 891	192.2	21.2	689	5	AG105245	C 964	191.8	21.1	390	8	BM988047
C 892	192.2	21.2	690	8	AO375664	C 965	191.8	21.1	432	8	AO047116
893	192.2	21.2	692	6	CA439730	C 966	191.8	21.1	432	8	AO047116
894	192.2	21.2	695	6	CA447325	C 967	191.8	21.1	437	2	BF448553
895	192.2	21.2	697	6	BI256839	C 968	191.8	21.1	459	8	AO150790
C 896	192.2	21.2	702	4	BI256839	C 969	191.8	21.1	501	8	AO588985
C 897	192.2	21.2	708	5	BU624395	C 970	191.8	21.1	507	7	CR558360
898	192.2	21.2	711	5	BU624395	C 971	191.8	21.1	512	5	BO029024
C 899	192.2	21.2	714	7	CN409711	C 972	191.8	21.1	538	5	BU584984
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					BX508704						
					BO632031						
					CN264754						
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					BQ883717						
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					BQ045015						
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					BE545742						
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					AO346199						
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					CA439937						
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					BM263248						
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					AO483308						
					BP205616						
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					BE276686						
					BM740671						
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					CN360036						
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					AO266645						
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					BU184851						
					AG105245						
					AO375664						
					CA439730	</					

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C1267	190.6	21.0	727	5	BU561234	C1340	190.2	21.0	477	8	AQ226326
C1268	190.6	21.0	753	1	AL691690	C1341	190.2	21.0	470	8	AQ632842
C1269	190.6	21.0	801	5	BQ214885	C1342	190.2	21.0	490	8	AQ432147
C1270	190.6	21.0	833	4	BG286471	C1343	190.2	21.0	494	7	BE080768
C1271	190.6	21.0	882	5	BQ228201	C1344	190.2	21.0	498	2	CR787110
C1272	190.6	21.0	890	4	BG163987	C1345	190.2	21.0	520	6	CA964754
C1273	190.6	21.0	895	2	BF674823	C1346	190.2	21.0	525	8	AQ082123
C1274	190.6	21.0	949	1	AL568770	C1347	190.2	21.0	528	8	BS5665
C1275	190.6	21.0	1065	4	BM454948	C1348	190.2	21.0	552	4	BI223275
C1276	190.6	21.0	1088	4	BM477840	C1349	190.2	21.0	564	5	BU860291
C1277	190.6	21.0	5108	3	HSMB02883	C1350	190.2	21.0	566	5	BU957747
C1278	190.6	21.0	8421	3	HSMB08381	C1351	190.2	21.0	570	8	AQ018599
C1279	190.4	21.0	398	1	AA857377	C1352	190.2	21.0	574	8	AQ050760
C1280	190.4	21.0	410	1	AI674290	C1353	190.2	21.0	577	8	BI4093
C1281	190.4	21.0	416	8	AQ140695	C1354	190.2	21.0	589	8	AQ041600
C1282	190.4	21.0	420	1	AA167656	C1355	190.2	21.0	601	5	BX504170
C1283	190.4	21.0	448	1	AI7471481	C1356	190.2	21.0	607	8	BZ603705
C1284	190.4	21.0	453	1	AI744830	C1357	190.2	21.0	607	9	AG018337
C1285	190.4	21.0	454	4	BG006718	C1358	190.2	21.0	613	7	W27084
C1286	190.4	21.0	481	1	AL704739	C1359	190.2	21.0	625	9	AG018336
C1287	190.4	21.0	487	1	AA618531	C1360	190.2	21.0	637	8	AQ423458
C1288	190.4	21.0	487	8	AQ425255	C1361	190.2	21.0	639	6	CA308017
C1289	190.4	21.0	492	8	AQ198722	C1362	190.2	21.0	663	1	AL709338
C1290	190.4	21.0	494	8	AQ392572	C1363	190.2	21.0	666	9	AG040280
C1291	190.4	21.0	502	8	AQ391359	C1364	190.2	21.0	666	9	AG182057
C1292	190.4	21.0	524	8	BZ611490	C1365	190.2	21.0	667	9	AG165154
C1293	190.4	21.0	552	8	AQ377725	C1366	190.2	21.0	672	1	AV648612
C1294	190.4	21.0	556	8	AQ008086	C1367	190.2	21.0	687	1	AI174827
C1295	190.4	21.0	569	8	AZ520604	C1368	190.2	21.0	695	9	AG178603
C1296	190.4	21.0	582	5	BP336447	C1369	190.2	21.0	699	7	CR789789
C1297	190.4	21.0	623	5	BU072384	C1370	190.2	21.0	706	9	AG133042
C1298	190.4	21.0	629	5	BQ786822	C1371	190.2	21.0	709	8	AO632003
C1299	190.4	21.0	655	9	AG134408	C1372	190.2	21.0	721	9	AG143216
C1300	190.4	21.0	657	8	AQ624700	C1373	190.2	21.0	721	9	AG085756
C1301	190.4	21.0	664	9	AG056105	C1374	190.2	21.0	828	8	BZ559498
C1302	190.4	21.0	667	9	AG159164	C1375	190.2	21.0	871	4	BI856069
C1303	190.4	21.0	668	9	AG146787	C1376	190.2	21.0	898	5	BU181297
C1304	190.4	21.0	679	9	AG159116	C1377	190.2	21.0	1049	5	AI572160
C1305	190.4	21.0	726	9	AG164176	C1378	190.2	21.0	1080	5	BQ213854
C1306	190.4	21.0	731	4	BM682955	C1379	190.2	21.0	1170	3	BC017436
C1307	190.4	21.0	732	4	CA427215	C1380	190.2	21.0	1805	3	CR621123
C1308	190.4	21.0	741	7	CR748203	C1381	190.2	21.0	1888	3	BC037885
C1309	190.4	21.0	759	5	BQ014487	C1382	190.2	21.0	385	8	AQ278103
C1310	190.4	21.0	769	5	BQ710315	C1383	190.2	20.9	412	1	AG192505
C1311	190.4	21.0	829	5	CB308284	C1384	190.2	20.9	412	1	AI735609
C1312	190.4	21.0	861	8	AQ897084	C1385	190.2	20.9	414	4	BG112362
C1313	190.4	21.0	877	5	BQ953835	C1386	190.2	20.9	420	7	CN277619
C1314	190.4	21.0	911	6	CD520000	C1387	190.2	20.9	424	4	BI324902
C1315	190.4	21.0	938	9	CL423157	C1388	190.2	20.9	431	1	AA015948
C1316	190.4	21.0	947	5	BQ707946	C1389	190.2	20.9	439	2	AAW45946
C1317	190.4	21.0	954	2	BE618927	C1390	190.2	20.9	445	1	AA748071
C1318	190.4	21.0	987	5	BX417024	C1391	190.2	20.9	466	8	AQ382614
C1319	190.4	21.0	1007	1	AL548632	C1392	190.2	20.9	469	8	AQ029854
C1320	190.4	21.0	1122	1	AL525584	C1393	190.2	20.9	479	7	CN276493
C1321	190.4	21.0	1306	3	BC022398	C1394	190.2	20.9	491	2	AAW469214
C1322	190.4	21.0	4050	3	CR749265	C1395	190.2	20.9	508	8	AQ418545
C1323	190.4	21.0	4086	3	HSMB07683	C1396	190.2	20.9	509	1	AI815210
C1324	190.4	21.0	4717	3	BC039267	C1397	190.2	20.9	529	4	BG407924
C1325	190.4	21.0	7180	3	HSMB04869	C1398	190.2	20.9	529	8	BI15895
C1326	190.2	21.0	318	7	NS5076	C1399	190.2	20.9	541	7	CN263446
C1327	190.2	21.0	344	1	AI708108	C1400	190.2	20.9	543	5	BU947632
C1328	190.2	21.0	355	1	AA349923	C1401	190.2	20.9	573	3	BU173705
C1329	190.2	21.0	369	1	AA084320	C1402	190.2	20.9	574	8	AQ820118
C1330	190.2	21.0	389	1	AI581006	C1403	190.2	20.9	588	7	CN344468
C1331	190.2	21.0	408	1	AI362442	C1404	190.2	20.9	588	4	BF977720
C1332	190.2	21.0	426	1	AI205783	C1405	190.2	20.9	619	8	AO545078
C1333	190.2	21.0	430	8	AQ270854	C1406	190.2	20.9	624	6	CA416290
C1334	190.2	21.0	433	2	BE005743	C1407	190.2	20.9	650	4	BG771029
C1335	190.2	21.0	436	8	BE0062816	C1408	190.2	20.9	684	8	BZ603428
C1336	190.2	21.0	448	4	BM672913	C1409	190.2	20.9	688	1	AV728560
C1337	190.2	21.0	453	8	AQ187593	C1410	190.2	20.9	699	1	AI905408
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BG286471	602382959										AQ632842
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BG163987	602343185										AQ432147
BF674823	602137982										HS_5050_A
AL568770	AL568770										BE080768
BM454948	AGENCOURT										QVI-BT063
BM477840	AGENCOURT										DKFP2469K
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BX482823	Homo sapi										1810C07.x
AA857377	od83g11.s										CA964754
AI674290	ct15C03.x										RPCT11-54
AQ140695	HS_3112.A										AG082123
AA167656	zq38f01.s										CT-HSP-200
AI7471481	ta20g07.s										602941310
AI744830	ct15f01.x										BU860291
BG006718	QV4-GN012										AGENCOURT
AL704739	DKFP26861										CT-HSP-2
AA618531	np38a03.s										AGENCOURT
AQ425255	CITBI-EI-										CT-HSP-2
AQ198722	RPCT11-59										AGENCOURT
AQ392572	CITBI-EI-										CT-HSP-2
AQ391359	CITBI-EI-										AGENCOURT
BZ611490	WHACSO6TP										RPCT-11-2
AQ377725	RPCT11-15										A.864HS_TP
AQ008086	HS_5299_A										CT-HSP-2
AZ520604	RPCT-11-3										DKFP2686P
BP336447	BP336447										WHADP21TR
BU072384	im46B06.x										Homo sapi
BQ786822	il50a07.x										20a9 Human
AG134408	Pan trogl										AG018336
AQ624700	CITBI-EI-										AG018337
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AG159164	Pan trogl										AG018336
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AG159116	Pan trogl										AG018336
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AL548632	AL548632										AG018336
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1412	190	20.9	708	6	CA418269	UI-H-FHO-
1413	190	20.9	708	6	CA423367	UI-H-FHO-
1414	190	20.9	723	1	AG009426	Homo sapi
1415	190	20.9	723	1	AL120616	DKF2P761H
1416	190	20.9	744	4	BS714274	602674962
1417	190	20.9	761	5	BS713385	UI-E-COI-
1418	190	20.9	791	8	BS611781	MHACP32TF
1419	190	20.9	816	8	BS774212	mcv87h09.
1420	190	20.9	852	5	BS358769	BS358769
1421	190	20.9	913	5	BQ220561	AGENCOURT
1422	190	20.9	922	7	CO648600	ILLUMIGEN
1423	190	20.9	1040	1	BS557347	AL539367
1424	190	20.9	1102	4	BS458632	BS557347
1425	190	20.9	1102	4	BS458632	AGENCOURT
1426	190	20.9	1603	3	CR592832	full-1eng
1427	190	20.9	1640	3	CR616737	full-1eng
1428	190	20.9	2594	3	CR624250	full-1eng
1429	190	20.9	2597	3	CR749260	Homo sapi
1430	190	20.9	6130	3	CR749575	Homo sapi
1431	189.8	20.9	352	5	BS752141	UI-1-BBO-
1432	189.8	20.9	359	8	AC002638	CIT978SK-
1433	189.8	20.9	363	4	BS710939	UI-E-DX1-
1434	189.8	20.9	368	1	AI537800	tp35e10.x
1435	189.8	20.9	393	8	BS774352	RPCL11-14
1436	189.8	20.9	398	5	BQ286595	ik32a06.x
1437	189.8	20.9	412	6	C75332	C75332
1438	189.8	20.9	413	1	AU160091	Huma
1439	189.8	20.9	438	1	AI973173	AI973173
1440	189.8	20.9	450	7	R70883	Y149C12..rl
1441	189.8	20.9	453	1	AI561058	nv75g10.r
1442	189.8	20.9	455	1	AA15876	DKF2P779D
1443	189.8	20.9	457	5	BSX503163	BSX503163
1444	189.8	20.9	458	5	BSX872813	BSX872813
1445	189.8	20.9	458	5	BSX875483	BSX875483
1446	189.8	20.9	459	7	R38879	YD06001..bl
1447	189.8	20.9	460	1	AI520693	C106d07.x
1448	189.8	20.9	464	6	BS156265	K-BSR0214
1449	189.8	20.9	466	1	AA890236	aj92d03..b
1450	189.8	20.9	469	2	BS675681	7E14a11.x
1451	189.8	20.9	477	8	AQ221138	HS 2258.B
1452	189.8	20.9	482	6	CR0455252	NISC.gc09
1453	189.8	20.9	487	1	AA554289	nk36f04.s
1454	189.8	20.9	499	5	BS991473	UI-H-DHO-
1455	189.8	20.9	517	8	AL706004	DKF2P686D
1456	189.8	20.9	517	8	AQ226976	HS 3220.A
1457	189.8	20.9	525	2	BS858746	7G04c03.x
1458	189.8	20.9	529	8	BS858746	7G04c03.x
1459	189.8	20.9	533	4	BSM04224	ih23b07.x
1460	189.8	20.9	537	1	AU155196	AU155196
1461	189.8	20.9	544	7	CV416475	RC3-GN007
1462	189.8	20.9	553	8	BZ605690	WHABD30TR
1463	189.8	20.9	554	5	BS116486	BS116486
1464	189.8	20.9	564	8	AQ114873	CIT-HSP-2
1465	189.8	20.9	567	1	AL047633	DKF2P586J
1466	189.8	20.9	568	5	BS265863	BS265863
1467	189.8	20.9	579	1	AI084785	g28D07..x
1468	189.8	20.9	584	5	BS276084	BS276084
1469	189.8	20.9	593	6	CA866953	1r75a10..x
1470	189.8	20.9	598	7	CN268101	170005318
1471	189.8	20.9	599	5	BS664046	c1110e10.
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1473	189.8	20.9	618	8	BZ601773	WHABH63TF
1474	189.8	20.9	620	5	BSU674398	UI-CF-DUO
1475	189.8	20.9	633	4	BM045087	603622955
1476	189.8	20.9	642	5	BSU783221	in04h06..x
1477	189.8	20.9	650	5	BSM977711	UI-H-DHO-
1478	189.8	20.9	657	8	BZ605279	WHABU08TF
1479	189.8	20.9	657	8	AG036674	Pan trogl
1480	189.8	20.9	694	4	BSG705001	602688991
1481	189.8	20.9	696	4	AG098088	Pan trogl
1482	189.8	20.9	704	5	BX100447	BX100447
1483	189.8	20.9	709	5	BS631944	UI-H-FBI-
1484	189.8	20.9	711	8	BS95096	CIT-HSP-217

1485	189.8	20.9	720	2	BS792793	BS792793
1486	189.8	20.9	739	4	BS529422	602558572
1487	189.8	20.9	744	6	CA417359	UI-H-FHO-
1488	189.8	20.9	746	6	CA428059	UI-H-DFO-
1489	189.8	20.9	768	4	BSM00265	BSM00265
1490	189.8	20.9	771	4	BS1334845	602998975
1491	189.8	20.9	779	2	BS666614	602121491
1492	189.8	20.9	786	5	BS0669133	BS0669133
1493	189.8	20.9	894	7	BS1084466	BS1084466
1494	189.8	20.9	913	7	CR455309	AGENCOURT
1495	189.8	20.9	923	8	AQ270526	HS 2046.B
1496	189.8	20.9	958	5	BS0588545	AGENCOURT
1497	189.8	20.9	961	4	BS133857	BS133857
1498	189.8	20.9	1027	5	BZ611225	WHACJ74TF
1499	189.8	20.9	1041	8	BQ277794	AGENCOURT
1500	189.8	20.9	1060	4	BSM78509	BSM78509

ALIGNMENTS

RESULT 1	CA427660/c	650 bp	mRNA	linear	EST 07-NOV-2002
LOCUS	UI-H-DFO-beo-o-24-0-UI.s1	NCI CGAP DFO	Homo sapiens	CDNA	clone
DEFINITION	UI-H-DFO-beo-o-24-0-UI 3', mRNA sequence.				
ACCESSION	CA427660				
VERSION	CA427660.1	GI:24790386			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 650)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Jose Mercuende cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu The following repetitive elements were found in this cDNA sequence: 15-303, >ALU (matched complement) 305-370, >MER64A (matched complement) Seq primer: M13 FORWARD PolyA=Yes.				

FEATURES

source	1..650	Location/Qualifiers
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
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	/tissue_type="Subchondral Bone"	
	/dev stage="Adult"	
	/lab host="D10B (Life Technologies)"	
	/clone.lib="NCI CGAP DFO"	
	/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DFO is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The	

sequence tag for this library is GTTAAAGCTC.

TAG_TISUB=Subchondral bone

TAG_LIB=UI-H-DP0

TAG_SBO=GTAAAGCTC"

ORIGIN

Query Match 67.9%; Score 616.2; DB 6; Length 650;
Best Local Similarity 99.4%; Pred. No. 7.4e-91;
Matches 629; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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OY 276 AGTCCACACACAGACTGGCGGAGGCGACAGAGGGGACAGATCTTGTGTGCTGGTTGA 335
DB AGTCCACACACAGACTGGCGGAGGCGACAGAGGGGACAGATCTTGTGTGCTGGTTGA 591
OY 336 CAGTAAAGGGGCTTGGCAGATCC-AGGTTGGGGGGGGCGGCAATCCCAATAAGAACCGA 394
DB CAGTAAAGGGGCTTGGCAGATCCAGATCCAGAGGGGGGGGGCGGCAATCCCAATAAGAACCGA 531
OY 395 GGGTCTGGGGCCCGGCGACAGAGTCACTGGCCAGCTCTGTGCTGTGGCCAGTGGAG 454
DB GGGTCTGGGGCCCGGCGACAGAGTCACTGGCCAGCTCTGTGCTGTGGCCAGTGGAG 471
OY 455 TGGCAGAGTGGGGCTTTGTGCGCAGTAAACCAAGGCTGATTTGCTGGGGCCATG 514
DB TGGCAGAGTGGGGCTTTGTGCGCAGTAAACCAAGGCTGATTTGCTGGGGCCATG 411
OY 515 GTCCCTGTCTAGGGGAGAGATTTCTCAACCTTGTCTGTCAAGAGCCCAAGAGCTTCA 574
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OY 575 TTGTATCTATTGATTTTACCAATTACCAATTAACTGAGAAATGGGCGGCGACCGT 634
DB TTGTATCTATTGATTTTACCAANTTAACTGAGAAATGGGCGGCGACCGT 291
OY 635 GGGTCAAGCTCTGTAATCCAGACATTTGGAGGGCGGAGGGCGGATCACTTGATCA 694
DB GGGTCAAGCTCTGTAATCCAGACATTTGGAGGGCGGAGGGCGGATCACTTGATCA 231
OY 695 GGAGTTCAAGACCGAGCTGGCGCAATGATGAAACCTTGTCTAATAAATAACAAAAT 754
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DB ATCGTTGAACCCAGAGAGCGGAGCTTGGCGGTGAGCGAGATCGCGCGCTGATTCCAGC 51
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DB CTGGGCGACAGAGTGAATCCATCTCACA 18
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RESULT 2
BP914480/c 470 bp mRNA linear EST 18-JAN-2001
LOCUS BP914480
DEFINITION IU3-UT0114-301100-358-E10 UT0114 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP914480
VERSION BP914480.1 GI:12305938
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 470)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IU3&ct=IU3-UT0114-
301100-358-E10&3=2000-11-30&t=41)
Seq primer: puc 18 forward
High quality sequence stop: 470.

FEATURES

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location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="UT0114"
/note="Organ: ureter tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 51.8%; Score 470; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 5.4e-67;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB AGATTAAGGAGGCGAGAGCCCTAGGGGAATGCTACCTCGCCCTTCACTGACCT 411
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DB GGTGTCAAGGTGCTGCTGCTCTCTGCGGAGAGAGTCTCTGCTGAGGAGCGAGA 351
OY 410 GTGTTCACGGTGGCTGCTGCTCTCTGCGGAGAGAGTCTCTGCTGAGGAGCGAGA 351
DB GTGTTCACGGTGGCTGCTGCTCTCTGCGGAGAGAGTCTCTGCTGAGGAGCGAGA 269
OY 210 GAGAGCTCAAGACTCAAGCTCTTGTTCAGAGAGCACTTGGCAAGTCCAGCGATG 269
DB GAGAGCTCAAGACTCAAGCTCTTGTTCAGAGAGCACTTGGCAAGTCCAGCGATG 291
OY 350 GAGAGCTCAAGACTCAAGCTCTTGTTCAGAGAGCACTTGGCAAGTCCAGCGATG 291
DB GAGAGCTCAAGACTCAAGCTCTTGTTCAGAGAGCACTTGGCAAGTCCAGCGATG 291
OY 270 GTCCGAGTCCACACAGACTGGCGGCGGAGGCGAGGAGGAGGAGTCTGTTGTGCTTG 329
DB GTCCGAGTCCACACAGACTGGCGGCGGAGGCGAGGAGGAGGAGTCTGTTGTGCTTG 231
OY 290 GTCCGAGTCCACACAGACTGGCGGCGGAGGCGAGGAGGAGGAGTCTGTTGTGCTTG 231
DB GTCCGAGTCCACACAGACTGGCGGCGGAGGCGAGGAGGAGGAGTCTGTTGTGCTTG 231
OY 330 GTTGAACAGTAAGAGGCTTGTGCGCAGTCCAGGCTGGGGGCGGCAATCTCAATAAGAA 389
DB GTTGAACAGTAAGAGGCTTGTGCGCAGTCCAGGCTGGGGGCGGCAATCTCAATAAGAA 171
OY 230 GTTGAACAGTAAGAGGCTTGTGCGCAGTCCAGGCTGGGGGCGGCAATCTCAATAAGAA 171
DB GTTGAACAGTAAGAGGCTTGTGCGCAGTCCAGGCTGGGGGCGGCAATCTCAATAAGAA 171
OY 390 CCAGAGGCTCTGGGCGGCGGCGACAGAGTCACTTGGCCAGCTCTTGTGCTGGCCAGT 449
DB CCAGAGGCTCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111
OY 170 CCAGAGGCTCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111
DB CCAGAGGCTCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 111
OY 450 GGGAGTGGCACAGAGTGGGGCTTGTGCGCAGTAAACCAAGGCTGATTTGCTGGCGGG 509
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OY 510 CCATGTCTCTGTCTAGGCGAGCAATTCACCTTCTGCTCTCAGAGAC 559
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RESULT 3

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LOCUS	BP915910				
DEFINITION	IL3-UT0114-081200-366-E06 UT0114 Homo sapiens cDNA, mRNA sequence.				
ACCESSION	BF915910				
VERSION	BF915910.1	GI:12307368			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 470)				
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.J.F., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20202663				
PUBMED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?IL3=IL3&t2=IL3-UT0114 081200-366-E06&t3=2000-12-08&t4=1) Seq primer: puc 18 forward High quality sequence stop: 455. Location/Qualifiers				
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	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/dev_string="Adult"				
	/clone_lib="UT0114"				
	/note="Organ: uterus,tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
ORIGIN					
Query Match	51.8%; Score 470; DB 2; Length 470;				
Best Local Similarity	100.0%; Pred. No. 5.4e-67;				
Matches	470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Gy	90 AGATAAAGGAGGAGGAGCCCAATGGGAATGTACTCTCGTCCCTTCACATGCCCT 149				
Db	470 AGATAAAGGAGGAGGAGCCCAATGGGAATGTACTCTCGTCCCTTCACATGCCCT 411				
Gy	150 GGTTGTCACGGTGCGCTGGTCCCTCTCTTCGCGAGAAGTGTCTTGCTGAGGAGGCAGA 209				
Db	410 GGTTGTCACGGTGCGCTGGTCCCTTCGCGAGAAGTGTCTTGCTGAGGAGGCAGA 351				
Gy	210 GGAGGCTCACAATCCACGACCCTTTGTTACGAGAGGAACATTGGCAAGGTCACAGCATG 269				
Db	350 GGAGGCTCACAATCCACGACCCTTTGTTACGAGAGGAACATTGGCAAGGTCACAGCATG 291				
Gy	270 GTCCGGAAGTCACACACAGACTGCGCGCACGGCAGAGGAGGAGACAGTTCTGTTGTGCTTG 329				
Db	290 GTCCGGAAGTCACACACAGACTGCGCGCACGGCAGAGGAGGAGACAGTTCTGTTGTGCTTG 231				
Gy	330 GTTGAACAGTAAGAGGCTTTGGCCAATGCACAGGTTGGGAGGCGCAACTCCATTAAGAA 389				

Db	230	GTTTGGACAGTAAAGGGTCTTTGGCCAGTCCAGGTGGGGGGCGGCAAACTCATTAAGAA	171
Qy	390	CCAGAGGGTCTGGGCCCCGGGCAACAGATCATCTGCCAGCTCTCTGTGTCGGCCAGT	449
Db	170	CCAGAGGGTCTGGGGCCCCGGGCAACAGATCATCTGCCAGCTCTCTGTGTCGGCCAGT	111
Qy	450	GGGAGTGGCACAGAGTGGGGGCTTTGGCCAGTAAACCAAGCTGGATTGGCTGGGG	509
Db	110	GGGAGTGGCACAGAGTGGGGGCTTTGGCCAGTAAACCAAGCTGGATTGGCTGGGG	51
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Db	50	CCATGGTCCCTGTCTAAGGAGCAAAATTCCTCAACCTTTCTCTCAGAC	1
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BP912836/c			
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DEFINITION	IL3-UT0114-221100-340-G10 UT0114 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BP912836		
VERSION	BP912836.1	GI:12304294	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 470) Das Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Marukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496	(2000)
MEDLINS	20202863		
PUBMED	10737800		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Rudwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/ILCR Human Cancer Genome Project. This entry can be seen in the following URL. (http://www.ludwig.org.br/bcstypes/gethtml2.pl?tl=IL3&t2=IL3-UT0114-221100-340-G10&t3=2000-11-22&t4=1) Seq primer: puc 18 forward High quality sequence stop: 470. Location/Qualifiers		
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source	1..470		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/dev_stage="Adult"		
	/clone_id="UT0114"		
	/note="Organ: uterine tumor; Vector: puc18; Site: 1; SmaI; Site:2; SmaI; A mini-library was made by cloning products derived from ORESTS PCR (U.S. Letters Patent applich) No.196,716 - Ludwig institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription ob tissue mRNA and cDNA amplification were performed under low stringency conditions."		
ORIGIN			
Query Match	51.7%	Score 469;	DB 2; Length 470;
Best Local Similarity	99.8%	Pred. No. 7,8e-67;	
Matches 469;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;

QY	90	GGATTAACGTGAGGGGAGGACCCCATTAAGGGAGAAATGCTACTCTGCTCTTCAACCTGACCCCT	149
Db	470	AGATTAACCTTGAAGGGAGGAGACCCCATTAAGGGAGAAATGCTACTCTGCTCTTCAACCTGACCCNT	411
QY	150	GGTGTTCACGGTGGCTGTGCTCTCTCTTGCCGAGAGAGTGTCTTGGGTCAAGGAGCGCAGA	209
Db	410	GGTGTTCACGGTGGCTGTGCTCTCTTGCCGAGAGAGTGTCTTGGGTCAAGGAGCGCAGA	351
QY	210	GGAAGCTCAACAGACTTCCAGCCCTTTGTATCCGAGAGGACACTTGGCCAAAGGTCCAGCCAGT	269
Db	350	GGAAGCTCAACAGACTTCCAGCCCTTTGTATCCGAGAGGACACTTGGCCAAAGGTCCAGCCAGT	291
QY	270	GTCCGGAATCCACACACAGACTGCGCGGAGGGCAGAGAGGGGGACAGTTCTGTGTGCTTG	329
Db	290	GTCCGGAATCCACACACAGACTGCGCGGAGGGCAGAGAGGGGGACAGTTCTGTGTGCTTG	231
QY	330	GTTGGACAGTAAAGAGGTTCTTGGCCAGTCCAGAGGTGGGGGGCGGCAAACTCCATAAAGAA	389
Db	230	GTTGGACAGTAAAGAGGTTCTTGGCCAGTCCAGAGGTGGGGGGCGGCAAACTCCATAAAGAA	171
QY	390	CCAGAGGGGTCTGGGGCCCGGGCCACAGATCATCTGSCCAGCTCCTCTGTGCTGGCCAGT	449
Db	170	CCAGAGGGGTCTGGGGCCCGGGCCACAGATCATCTGSCCAGCTCCTCTGTGCTGGCCAGT	111
QY	450	GGAGATGCAACGAGGTGGGGGCTTTGTGCAAGTAAACCAACAGGCTGGAATTTGCCCTGCGGG	509
Db	110	GGAGATGCAACGAGGTGGGGGCTTTGTGCAAGTAAACCAACAGGCTGGAATTTGCCCTGCGGG	51
QY	510	CCATAGTTCCTCTGTCTAAGGCAAGCAATTTCTCAACTCTTTGCTCTCAAGAC	559
Db	50	CCATAGTTCCTCTGTCTAAGGCAAGCAATTTCTCAACTCTTTGCTCTCAAGAC	1

RESULT	5
CBS985553	
LOCUS	
DEFINITION	792 bp mRNA linear EST 01-MAY-2003
	AGENCY/COURT 13671931 NIH_MGC_184 Homo sapiens CDNA clone
	IMAGE:30327377 5' mRNA sequence.

SOURCE ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 752)
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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Location/Qualifiers
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FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3037377"
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/clone_id="NTH_MGC_184"
/note="Organ: Pooled_Glandular_Vector: pDNR-LIB, Site_1:
SfiI (ggcgcctagcgc), Site_2: SfiI (ggcgcctagcgc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'

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adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCGCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCACGAGCGCGCGCATATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by NIM MGC laboratories (Palo Alto, CA). Note: this is a NIM MGC Library."

ORIGIN

Query Match	51.4%	Score 466.4	DB 6	Length 792
Best Local Similarity	95.7%	Pred. No. 1.7e-66		
Matches 534, Conservative	0	Mismatches 16	Indels 8	Gaps 5

QY	210	GGAGGCTCAGACATCCAGAGCCCTTTGGTATCCGAGAGACACTTGGCAAGGCTCAGCATG	265
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QY	270	GTCCGAGTCCACACACAGACTGGCCGAGGGCAGAGGGGGACAGTTCGTGTGCTTG	329
Db	97	GTCCGAGTCCACACAGACTGGCCGAGGGCAGAGGGGGACAGTTCGTGTGCTTG	156
QY	330	GTTGGAACGTAAAGGGGCTTTGGCAGTCCAGGGTGGGGGGCGCAAACTCCATAAAGAA	389
Db	157	GTTGGAACGTAAAGGGGCTTTGGCAGTCCAGGGTGGGGGGCGCAAACTCCATAAAGAA	216
QY	390	CCAAAGGTCCTGGGCCCCCGGCAAGAGTCACTGGCCAGCTCCTCGCTGGCCAGT	449
Db	217	CCAAAGGTCCTGGGCCCCCGGCAAGAGTCACTGGCCAGCTCCTCGCTGGCCAGT	276
QY	450	GGGAGTGCAAGAGGTGGGGCTTTGTGTCAGTAAACCAAGCGTGGATTGCTCGGG	509
Db	277	GGGAGTGCAAGAGGTGGGGCTTTGTGTCAGTAAACCAAGCGTGGATTGCTCGGG	336
QY	510	CCATGTCCTCTGTCTAAGGGCAGCAATTCTCAACTTTTGTCTCAGGACCCCAAGAGC	569
Db	337	CCATGTCCTCTGTCTAAGGGCAGCAATTCTCAACTTTTGTCTCAGGACCCCAAGAGC	396
QY	570	TTTCAATTGTATCTATATATATTTTTCACATTAGCAATTAA--CTGAGAAATGGGGCGG	627
Db	397	TTTCAATTGTATCTATATATATTTTTCACATTAGCAATTAAACTGAGAAATGGGGCGG	456
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Db	457	GCACGGTGGCTCAGCGCTGTATATCCAGCACTTTGGAGGGCCGAGAGGGGTGAATCACCC	516
QY	687	TGAGATCAGG-AGTTCAAGACAG-CTGGCCAAATGTGAAACTTTGTCT--ACTAA	741
Db	517	TGAGATCAGGAAGTTCAAGACACAGCCCTGGCCAAATGTGAAAACCTTGGTCACTTAA	576
QY	742	AAATTCAAAAAATTAGCC	759
Db	577	AAATTCAAAAAATTAGCC	594

LOCUS	DEFINITION	IMAGE:810034.5', mRNA sequence.	AA646988/C	AA646988	480 bp	RNA	linear	EST 10--JUN-1997
RESULT 6								

ACCESSION	AA464988
VERSION	AA464988.1
	GI:2189872

KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM Homo sapiens
 Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 480)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le N., Lennon, G., Marra, M., Martin, J.,

Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wolfe, T., Waterston, R. and Wilson, R.

TITLE	DATE	TIME	LOCATION	REMARKS
WashU-Merck EST Project 1997				


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Db      186  |||||GGCCAGACGTCATCTGCCCCAGCTCTCTGCTGCGCCAGTGGAGTGGACGAGGTGG 127
Oy      468  |||||GGCTTTGGCCAGTAAACCAACAGGCTGTGATTTGCTCTGGGCGCATGTCTCTGCTAGG 527
Db      126  |||||GGCTTTGGCCAGTAAACCAACAGGCTGTGATTTG-CTGGGGCCATGGTCTCTGCTAGG 68
Oy      528  GCAGCAATTTCTCAACCTTCTGCTCTGAGAGCCCAAGAGCTTTCATTGTATCTATTGA 587
Db      67  GCAGCAATTTCTCAACCTTCTGCTCTGAGAGCCCAAGAGCTTTCATTGTATCTATTGA 8
Oy      588  TTTTTCAC 594
Db      7  TTTTTCAC 1

RESULT 8
AA399124/c 402 bp mRNA linear EST 16-MAY-1997
LOCUS      z49a02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:725642 5', mRNA sequence.
ACCESSION AA399124
VERSION    AA399124.1 GI:2052862
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 402)
            Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kuubab,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
            Washu-Merck EST Project 1997
            Unpublished (1997)
TITLE      JOURNAL
COMMENT    Contact: Wilson RK
            Washington University School of Medicine
            444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 279.
FEATURES   source
            location/Qualifiers
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            /tissue_type="ovarian tumor"
            /lab_host="DH10B (ampicillin resistant)"
            /clone_lib="Soares ovary tumor NbHOT"
            /note="Organ: ovary; Vector: pRT73D (Pharmacia) with a
            modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTTACCAATCTGAAGTGGAGCGCGCGGTCTTTTCTTTTCTTTT 3'],
            double-stranded cDNA was size selected, ligated to Eco RI
            adapters (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of a modified pRT73 vector
            (Pharmacia). Library constructed by Bento Soares and
            M.Facima Bernaldo. "
ORIGIN
Query Match 40.7%; Score 369; DB 1; Length 402;
Best local similarity 99.3%; Pred. No. 1.6e-50;
Matches 402; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
Oy      190  TCTTGAGTCAAGGACGACGAGACGCTCAACAGCTCCAGCCCTTTGTTACCGAGAGACA 249
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Db      402  TCTTGAGTCAAGGACGACGAGACGCTCAACAGCTCCAGCCCTTTGTTACCGAGAGACA 343
Oy      250  CTTGGCAAGGTCGACGATGATCGGAGTCCACACACAGACTGGGCGCAGAGAGG 309
Db      342  CTTGGCAAGTCCAGCGATGATCGGAGTCCACACACAGACTGGGCGCAGAGAGG 283
Oy      310  GGAAGTTCCTGTTGCTGCTGTTGAGACATGAAGAGGCTTTGGCCAGTCAAGGTTGGG 369
Db      282  GGAAGTTCCTGTTGCTGCTGTTGAGACATGAAGAGGCTTTGGCCAGTCAAGGTTGGG 223
Oy      370  GCGGCAATCTCCATTAAGAACCAAGAGGTCGGGCCCCCGCCACAGAGTCATCGGCCAG 429
Db      222  GCGGCAATCTCCATTAAGAACCAAGAGGTCG-GGCCCCCGCCACAGAGTCATCGGCCAG 164
Oy      430  CTCCTCTGCTGCTGGCCAGTGGAGTGGACAGAGTGGGCTTTGTCAGTAAACAC 489
Db      163  CTCCTCTGCTGCTGGCCAGTGGAGTGGACAGAGTGGGCTTTGTCAGTAAACAC 104
Oy      490  AGGCTGATTTGCTCTGGGCGCATGTGCTCTGTAGGCGACAAATTCACCTTTG 549
Db      103  AGGCTGATTTG-CTGGGCGCAT-GTCCGTCTAGGGCAGCAATTCACCTTTG 46
Oy      550  CTCACAGACCCCAAGAGCTTTCATTGTATCTATTGATTTTAC 594
Db      45  CTCACAGACCCCAAGAGCTTTCATTGTATCTATTGATTTTAC 1

RESULT 9
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LOCUS      zv44d03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:756485 5', mRNA sequence.
ACCESSION AA481356
VERSION    AA481356.1 GI:2210908
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 360)
            Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kuubab,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
            Washu-Merck EST Project 1997
            Unpublished (1997)
TITLE      JOURNAL
COMMENT    Contact: Wilson RK
            Washington University School of Medicine
            444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 219.
FEATURES   source
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            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTTACCAATCTGAAGTGGAGCGCGCGGTCTTTTCTTTTCTTTT 3'],
            double-stranded cDNA was size selected, ligated to Eco RI
            adapters (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of a modified pRT73 vector

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ORIGIN

(Pharmacla). Library constructed by Bento Soares and
M.Fatima Bonaldo. "

```

Query Match      37.9%; Score 344.2; DB 1; Length 360;
Best Local Similarity 98.9%; Pred. No. 1.8e-46;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 360 TGTTCACGAGAGACACTTGGCAAGTCCAGAGTCCGAGTCCACACAGACTGG 301
QY 294 CGGCAAGGAGAGAGGAGGAGCACTTCTGTGCTGTGGTGGACAGTAAAGAGGCTCTTGGC 353
DB 300 CGGCAAGGAGAGAGGAGGAGCACTTCTGTGCTGTGGTGGACAGTAAAGAGGCTCTTGGC 241
QY 354 CAGTCCAGGAGTGGGGGGGGCGGCAACTCCATAAGAAACAGAGGGTCTGGGCCCGGCGAC 413
DB 240 CAGTCCAGGAGTGGGGGGGGCGGCAACTCCATAAGAAACAGAGGGTCTGGGCCCGGCGAC 182
QY 414 AGAGTCATCTGCCAGCTCTCTGTGCTGTGCGCAGTGGAGTGGACAGAGTGGGGCTTT 473
DB 181 AGAGTCATCTGCCAGCTCTCTGTGCTGTGCGCAGTGGAGTGGACAGAGTGGGGCTTT 122
QY 474 GTGCCAGTAAACCAAGGCTGATTTGCTGCGGGCCATGGTCCCTGTCTAGGGCAGCA 533
DB 121 GTGCCAGTAAACCAAGGCTGATTTGCTGCGGGCCATGGTCCCTGTCTAGGGCAGCA 62
QY 534 ATTCTCAACCTTCTGTGCTCTCAGAGACCCCAAGAGCTTTCATGATCATGATTTT 593
DB 61 ATTCTCAACCTTCTGTGCTCTCAGAGACCCCAAGAGCTTTCATGATCATGATTTT 2
QY 594 C 594
DB 1 C 1

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RESULT 10
BM854082 547 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0136380 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-145-D09
DEFINITION 5', mRNA sequence.

ACCESSION BM854082
VERSION BM854082.1 GI:19210481
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 547)
Kim,K.J., Hahn,Y.Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Kim,N.S., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

TITLE 21C Frontlter Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 145 row: D column: 09
High quality sequence stop: 547.

FEATURES

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ORIGIN

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Query Match      36.9%; Score 334.4; DB 4; Length 547;
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/note="Organ: Stomach; Vector: pT73-Pac; Site 1: EcorI;
Site 2: NotI; The S22SNUI6 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park U.G. et al.
(1990), Cancer Res 50: 2773-2780."

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QY 1 GGACTGGAAGGTCCCAAGAGCTGTGAGGCGCCCAAGAAAGTGTCCAACCTTGAGC 60
DB 212 GAACTGGAAGGTCCCAAGAGCTGTGAGGCGCCCAAGAAAGTGTCCAACCTTGAGC 271
QY 61 CCTAGAGGCTGTGATTTGTGCTGTTAAACAATTAACCTGAGGAGACCCCATAGGGGA 120
DB 272 CCTAGAGGCTGTGATTTGTGCTGTTAAACAATTAACCTGAGGAGACCCCATAGGGGA 331
QY 121 ATGCTACTCTGCTGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 332 ATGCTACTCTGCTGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 391
QY 181 GAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 392 GAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 451
QY 241 GAGAGACACTTGGCAAGGTCCAGAGTGTCCGAGTCCACACAGACTTGGCGCAGG 300
DB 452 GAGAGACACTTGGCAAGGTCCAGAGTGTCCGAGTCCACACAGACTTGGCGCAGG 511
QY 301 GCAGGAGGGGAGACAGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 336
DB 512 GCAGGAGGGGAGACAGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 547

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RESULT 11
BF963567/c
LOCUS PM1.NM1207-211200-013-d11 NM1207 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF963567
ACCESSION BF963567.1 GI:12380751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 511)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Coenca,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongseneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-NN1207-211200-013-d1&t3=2000-12-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 511.
Location/Qualifiers

FEATURES
SOURCE

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/notes="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORBESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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ORIGIN

Query Match 34.0%; Score 308; DB 4; Length 511;
Best Local Similarity 99.1%; Pred. No. 1.3e-40;
Matches 330; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db 369 GGACTCTGAAGGTCCAGAGAGCTGCTGAGGCCCCCAAGAGTGTTCACCTTGAC 310
Oy 61 CCTAGAGGGGTCTGATTTGCTGTTTAAACAAGTAACTGAGGGGAGAGCCCATAGGGGA 120
Db 309 CCTAGAGGGGTCTGATTTGCTGTTTAAACAAGTAACTGAGGGGAGAGCCCATAGGGGA 250
Oy 121 ATGCTACTCTGCTGCTTCCACCTGCTGCTGTTTACAGGTGGCCTGCTCTCTTGCC 180
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Oy 181 GAGAGAGTGTCTGGGTTCAGAGGAGCAGAGAGCTCAGACCTCCAGCCCTTTGTACC 240
Db 189 GAGAGAGTGTCTGGGTTCAGAGGAGCAGAGAGCTCAGACCTCCAGCCCTTTGTACC 130
Oy 241 GAGAGGACACTTGGCAAGGTCCAGAGATGTCGCGAGTCCACACACAGACTGGCGGACAG 300
Db 129 GAGAGGACACTT-GCAAGTCCAGAGATGTCGCGAGTCCACACAGACT-GCGGACAG 72
Oy 301 GCAGAGGGGGAGACAGTTCTGTGTGCTTGGTTG 333
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DEFINITION BI034628
ACCESSION BI034628
VERSION BI034628.1 GI:14441254
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 511)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brenani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
Sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-NN1207-050401-013-d1&t3=2001-04-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 511.
Location/Qualifiers

FEATURES
SOURCE

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1. 511
/organism="Homo sapiens"
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/notes="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORBESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
```

ORIGIN

Query Match 34.0%; Score 308; DB 4; Length 511;
Best Local Similarity 99.1%; Pred. No. 1.3e-40;
Matches 330; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Oy 1 GGACTCTGAAGGTCCAGAGAGCTGCTGAGGCCCCCAAGAGTGTTCACCTTGAC 60
Db 369 GGACTCTGAAGGTCCAGAGAGCTGCTGAGGCCCCCAAGAGTGTTCACCTTGAC 310
Oy 61 CCTAGAGGGGTCTGATTTGCTGTTTAAACAAGTAACTGAGGGGAGAGCCCATAGGGGA 120
Db 309 CCTAGAGGGGTCTGATTTGCTGTTTAAACAAGTAACTGAGGGGAGAGCCCATAGGGGA 250
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ACCESSION CN277578
VERSION CN277578.1 GI:472933992
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 308)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS	Brandenberger,R., Wei,H., Zhang,S., Lei,S., Wurage,J., Fisk,G.J., Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.					
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation					
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)					
COMMENT	Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 308 Std Error: 0.00. Location/Qualifiers 1..308 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7" /clone_id="GRN_PRENBU" /note="Oligo dt primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."					
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OY	602	GCAATTTAAACTGAGAAAATGGGCCCGGCACGGTGGCTACGCGCTGAATCCAGACATTT	661			
Db	61	GCAATTTAAACTGAGAAAATGGGCCCGGCACGGTGGCTACGCGCTGAATCCAGACATTT	120			
OY	662	GGGAGCGCGAGCGGGGTGATCAGCTGAGATCAGAGATTCAAGACCAAGCTGGCCAAT	721			
Db	121	GGGAGCGCGAGCGGGGTGATCAGCTGAGATCAGAGATTCAAGACCAAGCTGGCCAAT	180			
OY	722	GGTGAAACCTTGCTCTACTAAAAATACAAAAATTAGCCAGGACAGTGGTGTGACTGGT	781			
Db	181	GGTGAAACCTTGCTCTACTAAAAATACAAAAATTAGCCAGGACAGTGGTGTGACTGGT	240			
OY	782	AGTCCCAAGTACTCGGAGAGCTGAGGACGAGAAAATCGCTTGAACCCAGAGAGCGGACGTT	841			
Db	241	AGGCGCACGTTACTCGGAGAGCTGAGGACGAGAAAATCGCTTGAACCCAGAGAGCGGACGTT	300			
OY	842	GGCGTGAG 849				
Db	301	GGCGTAG 308				
RESULT 14						
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LOCUS	DKEPDP761H1914.t1.761 (synonym: hamy2)	Homo sapiens	cDNA clone			
DEFINITION	DKEPDP761H1914.5', mRNA sequence.					
ACCESSION	AL133867					
VERSION	AL133867.1	GI:6602054				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.					
AUTHORS	Angeorge,W., Warkner,U., Mewes,W., Well,B. and Wiemann,S.					
TITLE	EST (Angeorge,W., Warkner,U., Mewes,H.W., well,B. and Wiemann,S.) Unpublished (1999)					

COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de,
Heidelberg by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 81 sequence available.
This clone (DKFZp761H1914) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.

FEATURES
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location/Qualifiers
1..363
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Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 CGGGCAGCGTGGCTCAACGCTGTATATCCAGACTTTGGAGGCGGAGTGATCA 60

OY 685 CCGTAGATCAGAGGTTCAAGACCAAGCCTGCGCAACATGTTGTAACCTTTCTTAAAA 744
61 CCGTAGATCAGAGGTTCAAGACCAAGCCTGCGCAACATGTTGTAACCTTTCTTAAAA 120

OY 745 TACAAAAAATTAGCCAGGACACAGTGTGTGACGTGTATCCAGTTACTCGGAGGCTG 804
121 TACAAAAAATTAGCCAGGACACAGTGTGTGACGTGTATCCAGTTACTCGGAGGCTG 180

DB 805 AGGCAGAAAAATCGCTTAACCCAGAGGCGGAGCGTTGCGGTGAGCCGAGATCGCGCGC 864
181 AGGCAGAAAAATCGCTTAACCCAGAGGCGGAGCGTTGCGGTGAGCCGAGATCGCGCGC 240

OY 865 TGATTCCAGCCTGGGCGACAGAGTGAGACTTCATCTCACA 907
241 TGATTCCAGCCTGGGCGACAGAGTGAGACTTCATCTCACA 283

DB

RESULT 15
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LOCUS PM1-MT0198-191200-007-d11 MT0198 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF903767
VERSION BF903767.1 GI:12295226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 319)
Dlae Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Birones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. U., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663

JOURNAL
MEDLINE

PUBMED
COMMENT

10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&tl2=PM1-MT0198-
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Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 319.
Location/Qualifiers

FEATURES
source

1. 319
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/dev_stage="Adult"
/clone_lib="MT0198"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 29.9%; Score 271.2; DB 2; Length 319;
Best Local Similarity 92.8%; Pred. No. 1.5e-34;
Matches 295; Conservative 0; Mismatches 21; Indels 2; Gaps 1;

45 GATTCCAACTTGAACCCCTAGGGGTCTGATTGCTGTTAACAAGATAAATTGAGGGC 104
Db GTTCCAACCTTGAACCCCTAGGGGTCTGATTGCTGTTAACAAGATAAATTGAGGGC 260
QY 105 AGGACCCCATAGGGGAATGCTAATCTCTGCTTCCACTGCTGCTGCTTCAAGGTGGC 164
Db 259 AGGACCCCATAGGGGAATGCTAATCTCTGCTTCCACTGCTGCTGCTTCAAGGTGGC 200
QY 165 CTGGTCCCTCTTGGCCGAGAGATGTCCTGGGTCAAGGACGAGACGCTCAAGACT 224
Db 199 CTGGTCCCTCTTGGCCGAGAGATGTCCTGGGTCAAGGACGAGACGCTCAAGACT 140
QY 225 CCAGCCCTTTGTTACCGAGAGACAATTGGCAAGGTCCAGCATGTCTCCGAGTCCAC 284
Db 139 CCAGCCCTTTGTTACCGAGAGACAATTGGCAAGGTCCAGCATGTCTCCGAGTCCAC 80
QY 285 ACA--GACTGGCGGAGGCGAGAGGGGAGACATTCTGTGTGCTTGGTTGACAGTAAG 342
Db 79 ACATGACTGGCGGAGGCGAGAGGGGAGACATTCTGTGTGCTTGGTTGACAGTAAG 20
QY 343 AGGCTTTGGCCAGTCCA 360
Db 19 AGGCTCATTTGCCAATTCA 2

Search completed: September 15, 2005, 18:10:57
Job time : 3919 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 15:49:33 ; Search time 4378 Seconds
(without alignments)
10038.575 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 907

Sequence: 1 ggactctgaagtcacgaac.....gtgagactcattccacaca 907

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database:

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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	907	100.0	907 6 AR252642	AR252642 Sequence
2	907	100.0	907 6 AX358844	AX358844 Sequence
3	907	100.0	907 6 AX362337	AX362337 Sequence
4	907	100.0	907 6 AX403511	AX403511 Sequence
5	907	100.0	907 9 AY358690	AY358690 Homo sapi
6	907	100.0	907 9 AC105210	AC105210 Homo sapi
7	907	100.0	907 9 AC067930	AC067930 Homo sapi
8	907	100.0	907 9 AC019122	AC019122 Homo sapi
9	899	99.1	164959 2 AC087823	AC087823 Homo sapi
10	500	55.1	500 6 AR129215	AR129215 Sequence
11	458	50.3	480 6 CQ462746	CQ462746 Sequence
12	403	44.4	425 6 CQ460389	CQ460389 Sequence
13	369	40.7	402 6 CQ460821	CQ460821 Sequence
14	344.2	37.9	360 6 CQ463335	CQ463335 Sequence
15	232.8	24.6	399 6 AX071596	AX071596 Sequence
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17	217.6	24.0	321519 2 AL714004	AL714004 Homo sapi
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20	215.2	23.7	178964 2	AC150199	AC150199 Papio anu
21	214.6	23.7	155941 9	HS277C14	AL121984 Human DNA
22	214.6	23.7	168558 9	AC006948	AC006948 Homo sapi
23	214.4	23.6	93033 2	AP000644	AP000644 Homo sapi
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25	214	23.6	194020 9	HUAC004125	AC004125 Homo sapi
26	213.8	23.6	485 9	AY190787	AY190787 Gorilla g
27	213.8	23.6	81410 9	AP004715	AP004715 Homo sapi
28	213.8	23.6	101768 9	AC006465	AC006465 Homo sapi
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66	212.2	23.4	227245 9	AC008569	AC008569 Homo sapi
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68	212	23.4	104135 9	AC113373	AC113373 Homo sapi
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85	211.4	23.3	118994 9	AL139823	AL139823 Human DNA
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89	211.4	23.3	240699 9	AC146154	AC146154 Pan trogl
90	211.2	23.3	1973 9	AK130331	AK130331 Homo sapi
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94	211.2	23.3	168716	9	AC021299	AC021299 Homo sapi	c 167	209.2	23.1	59065	6	AR213191
95	211.2	23.3	173213	2	AC073865	AC073865 Homo sapi	c 168	209.2	23.1	62846	2	AC023982
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97	211	23.3	175664	9	AC027811	AC027811 Homo sapi	c 170	209.2	23.1	89747	9	AL591022
98	210.8	23.2	153225	2	AC013581	AC013581 Homo sapi	c 171	209.2	23.1	99486	9	AC008938
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c 117	210.2	23.2	104395	9	AC092469	AC092469 Homo sapi	c 190	209.2	23.0	62550	2	AC090460
c 118	210.2	23.2	160001	2	AC125515	AC125515 Pan trogl	c 191	209.2	23.0	73322	2	AC069380
c 119	210	23.2	301	6	AX741027	AX741027 Sequence	c 192	209.2	23.0	84323	9	HS13887
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c 126	209.8	23.1	68692	2	AP003163	AP003163 Homo sapi	c 199	209.2	23.0	161990	2	AL357313
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c 143	209.6	23.1	102313	9	AL603749	AL603749 Human DNA	c 216	208.8	23.0	153392	9	AL133548
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c 147	209.6	23.1	166258	2	AL451066	AL451066 Homo sapi	c 220	208.8	23.0	172600	9	AL359644
c 148	209.6	23.1	167548	9	AL1391809	AL1391809 Human DNA	c 221	208.8	23.0	173364	2	AC009807
c 149	209.6	23.1	184591	9	AL355443	AL355443 Human DNA	c 222	208.8	23.0	173472	2	AC144466
c 150	209.6	23.1	206246	2	AL606485	AL606485 Homo sapi	c 223	208.8	23.0	193168	2	AC011569
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c 154	209.4	23.1	108508	9	AC133539	AC133539 Homo sapi	c 227	208.6	23.0	111104	9	AC117389
c 155	209.4	23.1	147878	9	AC024600	AC024600 Homo sapi	c 228	208.6	23.0	120725	9	AC084123
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242	208.6	23.0	180237	9	AC091100	AC091100	Human sapi	315	207.8	22.9	80743	9	AC073422	AC073422	Human sapi
243	208.6	23.0	181853	9	CNS05TEN	AL359225	Human chr	316	207.8	22.9	132290	9	AL627402	AL627402	Human DNA
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252	208.6	23.0	205307	2	AC002928	AC022220	Human sapi	325	207.8	22.9	156615	9	AC008511	AC008511	Human sapi
253	208.6	23.0	232321	2	AC022220	AC092298	Human sapi	326	207.8	22.9	160770	9	AC008511	AC008511	Human sapi
254	208.4	23.0	437375	9	AC008238	AC008238	Human sapi	327	207.8	22.9	161740	2	AC084473	AC084473	Human sapi
255	208.4	23.0	74932	9	AC008762	AC008762	Human sapi	328	207.8	22.9	163969	2	BX284623	BX284623	Human sapi
256	208.4	23.0	115345	9	AC008147	AC008147	Human sapi	329	207.8	22.9	166181	9	HS375E16	HS375E16	Human sapi
257	208.4	23.0	131977	9	AC124857	AC124857	Human sapi	330	207.8	22.9	171411	2	AC0087609	AC0087609	Human sapi
258	208.4	23.0	131967	9	AL161622	AL161622	Human sapi	331	207.8	22.9	177573	2	AC019076	AC019076	Human sapi
259	208.4	23.0	132805	9	HS139A13	297054	Human DNA	332	207.8	22.9	181265	9	AC019356	AC019356	Human sapi
260	208.4	23.0	148429	2	HS139A13	AL109851	Human sapi	333	207.8	22.9	184111	9	AC008821	AC008821	Human sapi
261	208.4	23.0	179627	9	AC113426	AC113426	Human sapi	334	207.8	22.9	190765	9	AL359763	AL359763	Human sapi
262	208.4	23.0	197000	2	AC124859	AC124859	Human sapi	335	207.8	22.9	210799	2	AC013721	AC013721	Human sapi
263	208.4	23.0	207751	2	AC121819	AC008902	Human sapi	336	207.8	22.9	254633	2	CH762389	CH762389	Human sapi
264	208.2	23.0	101352	9	AC008902	AL136531	Human DNA	337	207.6	22.9	31766	6	AX354725	AX354725	Sequence
265	208.2	23.0	119072	9	AL136531	AC0084139	Human sapi	338	207.6	22.9	34346	9	AC0090632	AC0090632	Human sapi
266	208.2	23.0	126231	9	AC0084139	AC0084139	Human sapi	339	207.6	22.9	38852	9	AC006261	AC006261	Human sapi
267	208.2	23.0	131930	9	AC008925	AC008925	Human sapi	340	207.6	22.9	62319	2	AC132200	AC132200	Human sapi
268	208.2	23.0	133867	9	AL353648	AL353648	Human DNA	341	207.6	22.9	113456	9	HS1499B10	HS1499B10	Human sapi
269	208.2	23.0	141923	2	AC109997	AC109997	Human sapi	342	207.6	22.9	129430	9	AC008905	AC008905	Human sapi
270	208.2	23.0	144676	9	HS390013	284469	Human DNA	343	207.6	22.9	129719	9	AL358113	AL358113	Human sapi
271	208.2	23.0	145385	9	AL1732602	AL1732602	Human sapi	344	207.6	22.9	134793	9	AC020922	AC020922	Human sapi
272	208.2	23.0	147364	9	AC110998	AC110998	Human sapi	345	207.6	22.9	137922	2	AC073398	AC073398	Human sapi
273	208.2	23.0	147364	2	AC069480	AC069480	Human sapi	346	207.6	22.9	143756	9	AC136365	AC136365	Human sapi
274	208.2	23.0	163149	2	CNS01DS2	AL122057	Human chr	347	207.6	22.9	149577	9	AP005902	AP005902	Human sapi
275	208.2	23.0	163705	9	AC023774	AC023774	Human sapi	348	207.6	22.9	150140	2	AC005478	AC005478	Human sapi
276	208.2	23.0	163830	2	AC068235	AC068235	Human sapi	349	207.6	22.9	151851	2	AC009157	AC009157	Human sapi
277	208.2	23.0	163876	2	AC016402	AC016402	Human sapi	350	207.6	22.9	157850	9	AC034303	AC034303	Human sapi
278	208.2	23.0	169326	9	AC009783	AC009783	Human sapi	351	207.6	22.9	163567	2	AL365325	AL365325	Human sapi
279	208.2	23.0	171637	9	AC114876	AC114876	Human sapi	352	207.6	22.9	164607	9	AC022001	AC022001	Human sapi
280	208.2	23.0	174591	9	AC109335	AC109335	Human sapi	353	207.6	22.9	164846	9	AC145750	AC145750	Human sapi
281	208.2	23.0	174768	2	AC079191	AC079191	Human sapi	354	207.6	22.9	165761	2	AC145750	AC145750	Human sapi
282	208.2	23.0	186750	2	AC146199	AC146199	Human sapi	355	207.6	22.9	165770	9	AC023396	AC023396	Human sapi
283	208.2	23.0	187514	2	AC019267	AC019267	Human sapi	356	207.6	22.9	169598	9	AC087650	AC087650	Human sapi
284	208.2	23.0	184523	9	AC018642	AC018642	Human sapi	357	207.6	22.9	171007	2	AC131095	AC131095	Human sapi
285	208.2	23.0	194523	9	AC009712	AC009712	Human sapi	358	207.6	22.9	173627	9	AC099511	AC099511	Human sapi
286	208.2	23.0	213745	9	AC009481	AC009481	Human sapi	359	207.6	22.9	174612	9	AC018494	AC018494	Human sapi
287	208.2	23.0	227137	9	AC004388	AC004388	Human sapi	360	207.6	22.9	176584	2	AC062010	AC062010	Human sapi
288	208.2	23.0	243041	6	AX335303	AX335303	Sequence	361	207.6	22.9	177834	2	AC018811	AC018811	Human sapi
289	208.2	22.9	291	6	AX337621	AX337621	Sequence	362	207.6	22.9	179168	2	AC034283	AC034283	Human sapi
290	208.2	22.9	291	12	HSU14573	U14573	***ALU WARM	363	207.6	22.9	179168	2	AC009071	AC009071	Human sapi
291	208.2	22.9	43288	9	HS361A3	AL031717	Human DNA	364	207.6	22.9	179652	2	AC149616	AC149616	Human sapi
292	208.2	22.9	79516	9	AC004834	AC004834	Human sapi	365	207.6	22.9	182643	2	AP002794	AP002794	Human sapi
293	208.2	22.9	88029	9	AC004938	AC004938	Human sapi	366	207.6	22.9	185029	9	AC090707	AC090707	Human sapi
294	208.2	22.9	91907	9	AC131566	AC031566	Human sapi	367	207.6	22.9	188833	9	HS268H5	HS268H5	Human sapi
295	208.2	22.9	98433	9	AC097483	AC097483	Human sapi	368	207.6	22.9	189098	2	AC150627	AC150627	Human sapi
296	208.2	22.9	117335	9	AC093171	AC093171	Human sapi	369	207.6	22.9	191162	9	AC008865	AC008865	Human sapi
297	208.2	22.9	117335	9	AC004883	AC004883	Human sapi	370	207.6	22.9	193645	2	AC015951	AC015951	Human sapi
298	208.2	22.9	131359	9	AC134616	AC134616	Human sapi	371	207.6	22.9	198960	9	AC010145	AC010145	Human sapi
299	208.2	22.9	136431	9	AC136975	AC136975	Human sapi	372	207.6	22.9	204082	9	AC005323	AC005323	Human sapi
300	208.2	22.9	159229	2	AC116973	AC116973	Human sapi	373	207.4	22.9	8596	9	AL159581	AL159581	Human sapi
301	208.2	22.9	159604	2	AC083884	AC083884	Human sapi	374	207.4	22.9	27264	9	AC140753	AC140753	Human sapi
302	208.2	22.9	172033	9	AL136131	AL136131	Human DNA	375	207.4	22.9	43599	9	HS206C7	HS206C7	Human sapi
303	208.2	22.9	172237	2	AC131389	AL131389	Human sapi	376	207.4	22.9	47877	9	AC117438	AC117438	Human sapi
304	208.2	22.9	176141	9	AC138783	AC138783	Human sapi	377	207.4	22.9	96545	9	AC117438	AC117438	Human sapi
305	208.2	22.9	177322	9	AC002168	AC002168	Human sapi	378	207.4	22.9	122292	9	AC093535	AC093535	Human sapi
306	208.2	22.9	186210	9	AC007596	AC007596	Human sapi	379	207.4	22.9	132710	9	AL359707	AL359707	Human sapi
307	208.2	22.9	192473	2	AC079415	AC079415	Human sapi	380	207.4	22.9	142085	9	AL6273196	AL6273196	Human sapi
308	208.2	22.9	192473	2	AC124781	AC124781	Human sapi	381	207.4	22.9	147246	2	AC023196	AC023196	Human sapi
309	208.2	22.9	211531	9	AC006595	AC006595	Human sapi	382	207.4	22.9	156348	9	AC099513	AC099513	Human sapi
310	208.2	22.9	246322	2	AC133966	AC133966	Human sapi	383	207.4	22.9	158560	9	AC098669	AC098669	Human sapi
311	208.2	22.9	270150	9	AE006639	AE006639	Human sapi	384	207.4	22.9	165616	9	AC073333	AC073333	Human sapi

385	207.4	22.9	169554	2	AC021379	AC021379 Homo sapi	458	207	22.8	217615	2	AC083976	AC083976 Homo sapi
386	207.4	22.9	174535	2	AC106872	AC106872 Homo sapi	459	207	22.8	227912	2	AC138900	AC138900 Homo sapi
387	207.4	22.9	182488	2	AC036167	AC036167 Homo sapi	460	207	22.8	241781	2	AC145097	AC145097 Homo sapi
388	207.4	22.9	183976	2	AC100821	AC100821 Homo sapi	461	207	22.8	250483	2	AC145096	AC145096 Homo sapi
389	207.4	22.9	185571	9	AC133781	AC133781 Homo sapi	462	206.8	22.8	69201	9	AC004109	AC004109 Homo sapi
390	207.4	22.9	185602	2	AL139081	AL139081 Human DNA	463	206.8	22.8	77425	9	AF068862	AF068862 Homo sapi
391	207.4	22.9	188296	2	AC022324	AC022324 Homo sapi	464	206.8	22.8	88295	9	AC004612	AC004612 Homo sapi
392	207.4	22.9	188470	2	AC093005	AC093005 Homo sapi	465	206.8	22.8	89352	9	AC006030	AC006030 Homo sapi
393	207.4	22.9	191154	2	AC132150	AC132150 Homo sapi	466	206.8	22.8	99108	9	AC008665	AC008665 Homo sapi
394	207.4	22.9	193894	9	AC114730	AC114730 Homo sapi	467	206.8	22.8	104148	9	AC006146	AC006146 Homo sapi
395	207.4	22.9	196292	9	CNS0000B	AL049829 Human chr	468	206.8	22.8	116004	9	AF258545	AF258545 Homo sapi
396	207.4	22.9	200711	2	AC133960	AC133960 Homo sapi	469	206.8	22.8	121717	9	AL144548	AL144548 Human DNA
397	207.4	22.9	206587	2	AL138898	AL138898 Human DNA	470	206.8	22.8	138682	9	AL1731574	AL1731574 Human DNA
398	207.4	22.9	207983	9	AC009960	AC009960 Homo sapi	471	206.8	22.8	149790	9	AC022106	AC022106 Homo sapi
399	207.4	22.9	219821	9	AC008738	AC008738 Homo sapi	472	206.8	22.8	154577	2	AL357046	AL357046 Homo sapi
400	207.2	22.8	47167	9	HS757P12	AL031007 Human DNA	473	206.8	22.8	161164	2	AC022278	AC022278 Homo sapi
401	207.2	22.8	57084	2	AC129892	AC129892 Homo sapi	474	206.8	22.8	162728	9	AP002906	AP002906 Homo sapi
402	207.2	22.8	77880	9	AC114766	AC114766 Homo sapi	475	206.8	22.8	164906	9	AC096637	AC096637 Homo sapi
403	207.2	22.8	93847	9	AL157373	AL157373 Human DNA	476	206.8	22.8	168640	9	AC123779	AC123779 Homo sapi
404	207.2	22.8	100719	9	BX255925	BX255925 Human DNA	477	206.8	22.8	172614	9	AL929302	AL929302 Human DNA
405	207.2	22.8	121909	9	HS0492P14	AL121977 Human DNA	478	206.8	22.8	173403	9	BS000114	BS000114 Pan trogl
406	207.2	22.8	130526	2	AP000715	AP000715 Homo sapi	479	206.8	22.8	174521	2	AC127468	AC127468 Papio anu
407	207.2	22.8	138846	2	AC068478	AC068478 Homo sapi	480	206.8	22.8	175802	9	AC040174	AC040174 Homo sapi
408	207.2	22.8	147534	9	AC068620	AC068620 Homo sapi	481	206.8	22.8	176629	9	AC008641	AC008641 Homo sapi
409	207.2	22.8	151889	9	AC084250	AC084250 Homo sapi	482	206.8	22.8	177257	2	AL807789	AL807789 Homo sapi
410	207.2	22.8	154639	2	AC090175	AC090175 Homo sapi	483	206.8	22.8	184886	9	AC016650	AC016650 Homo sapi
411	207.2	22.8	167102	9	AC084017	AC084017 Homo sapi	484	206.8	22.8	185257	9	AL355305	AL355305 Human DNA
412	207.2	22.8	170722	9	AC087847	AC087847 Homo sapi	485	206.8	22.8	193132	2	AC025743	AC025743 Homo sapi
413	207.2	22.8	170877	2	AC025610	AC025610 Homo sapi	486	206.8	22.8	196772	2	AC087392	AC087392 Homo sapi
414	207.2	22.8	171035	9	AC016178	AC016178 Homo sapi	487	206.8	22.8	199208	2	AC019236	AC019236 Homo sapi
415	207.2	22.8	172403	2	AC017061	AC017061 Homo sapi	488	206.8	22.8	205819	2	AC106805	AC106805 Homo sapi
416	207.2	22.8	178917	9	AC021205	AC021205 Homo sapi	489	206.8	22.8	208953	9	CNS01RH3	AL160314 Human chr
417	207.2	22.8	183436	2	AC012489	AC012489 Homo sapi	490	206.8	22.8	331864	9	AF049895	AF049895 Homo sapi
418	207.2	22.8	193981	9	AC148832	AC148832 Pan trogl	491	206.6	22.8	433919	9	AL446023	AL446023 Human DNA
419	207.2	22.8	202856	2	AC027374	AC027374 Homo sapi	492	206.6	22.8	57494	9	BS000189	BS000189 Pan trogl
420	207.2	22.8	210133	9	AC013564	AC013564 Homo sapi	493	206.6	22.8	70148	9	AL357061	AL357061 Human DNA
421	207	22.8	2466	9	DB9927	DB9927 Human Na+/p	494	206.6	22.8	76792	9	AC023161	AC023161 Homo sapi
422	207	22.8	38906	9	BX842243	BX842243 Homo sapi	495	206.6	22.8	83731	2	AC079747	AC079747 Homo sapi
423	207	22.8	39852	9	AC006128	AC006128 Homo sapi	496	206.6	22.8	96608	9	HS308113	HS308113 Homo sapi
424	207	22.8	41630	9	AC005785	AC005785 Homo sapi	497	206.6	22.8	101861	2	AL359086	AL359086 Homo sapi
425	207	22.8	46775	9	HS0738A13	AL109801 Human DNA	498	206.6	22.8	107438	9	AC005281	AC005281 Homo sapi
426	207	22.8	65128	9	AC073188	AC073188 Homo sapi	499	206.6	22.8	113109	9	HS475N16	HS475N16 Homo sapi
427	207	22.8	76354	9	AC048340	AC048340 Homo sapi	500	206.6	22.8	116879	9	AC106854	AC106854 Homo sapi
428	207	22.8	78167	9	AC092028	AC092028 Homo sapi	501	206.6	22.8	120491	9	AC008859	AC008859 Homo sapi
429	207	22.8	85787	9	AC073069	AC073069 Homo sapi	502	206.6	22.8	127883	9	AL136141	AL136141 Human DNA
430	207	22.8	87386	9	AC133750	AC133750 Homo sapi	503	206.6	22.8	129577	9	AC004659	AC004659 Homo sapi
431	207	22.8	87758	9	AC068768	AC068768 Homo sapi	504	206.6	22.8	141000	9	AC121756	AC121756 Homo sapi
432	207	22.8	110000	2	AC140129	AC140129 Homo sapi	505	206.6	22.8	143060	9	AL929472	AL929472 Human DNA
433	207	22.8	111312	9	AC011248	AC011248 Homo sapi	506	206.6	22.8	147545	9	AC126614	AC126614 Homo sapi
434	207	22.8	118312	2	AC055713	AC055713 Homo sapi	507	206.6	22.8	148271	9	AL392046	AL392046 Human DNA
435	207	22.8	121353	2	AC033386	AC033386 Homo sapi	508	206.6	22.8	154754	9	AC064836	AC064836 Homo sapi
436	207	22.8	123529	9	AF179296	AF179296 Homo sapi	509	206.6	22.8	158078	9	AC005094	AC005094 Homo sapi
437	207	22.8	127867	9	HS694B14	AL1031673 Human DNA	510	206.6	22.8	160723	9	AC010722	AC010722 Homo sapi
438	207	22.8	132323	9	AC116615	AC116615 Homo sapi	511	206.6	22.8	160981	9	AC103986	AC103986 Homo sapi
439	207	22.8	139384	2	AC006455	AC006455 Homo sapi	512	206.6	22.8	161421	2	AC026649	AC026649 Homo sapi
440	207	22.8	149058	2	AC023065	AC023065 Homo sapi	513	206.6	22.8	163972	9	AC103987	AC103987 Homo sapi
441	207	22.8	152878	2	AC079190	AC079190 Homo sapi	514	206.6	22.8	167998	9	AL353662	AL353662 Human DNA
442	207	22.8	171897	9	AC145098	AC145098 Homo sapi	515	206.6	22.8	169736	2	AC019305	AC019305 Homo sapi
443	207	22.8	173391	9	AC090063	AC090063 Homo sapi	516	206.6	22.8	171990	9	AL137071	AL137071 Human DNA
444	207	22.8	174530	2	AL158835	AL158835 Human DNA	517	206.6	22.8	172868	9	AC009117	AC009117 Homo sapi
445	207	22.8	179759	2	AC132868	AC132868 Homo sapi	518	206.6	22.8	173766	9	AC004049	AC004049 Homo sapi
446	207	22.8	181864	2	AL353743	AL353743 Human DNA	519	206.6	22.8	175827	9	AL358472	AL358472 Human DNA
447	207	22.8	191280	2	AC087389	AC087389 Homo sapi	520	206.6	22.8	177444	9	AC011468	AC011468 Homo sapi
448	207	22.8	193519	2	AC023123	AC023123 Homo sapi	521	206.6	22.8	178384	2	AL591026	AL591026 Homo sapi
449	207	22.8	201886	2	AC140511	AC140511 Homo sapi	522	206.6	22.8	180166	2	AC011898	AC011898 Homo sapi
450	207	22.8	209859	2	AC084083	AC084083 Homo sapi	523	206.6	22.8	183048	2	AC011656	AC011656 Homo sapi
451	207	22.8	209870	2	AC104431	AC104431 Homo sapi	524	206.6	22.8	185688	2	AC018805	AC018805 Homo sapi
452	207	22.8	211810	2	AC026112	AC026112 Homo sapi	525	206.6	22.8	187174	9	AC006241	AC006241 Homo sapi
453	207	22.8	213861	9	AL135793	AL135793 Human DNA	526	206.6	22.8	191960	9	AC024475	AC024475 Homo sapi
454	207	22.8	215808	9	AC140179	AC140179 Homo sapi	527	206.6	22.8	196203	9	AL355355	AL355355 Homo sapi
455	207	22.8	215936	9	CNS0507CA	AL1355076 Human chr	528	206.6	22.8	200464	2	AC148619	AC148619 Macaca mu
456	207	22.8	216749	9	AC104319	AC104319 Homo sapi	529	206.6	22.8	204793	2	AC026333	AC026333 Homo sapi
457	207	22.8	216789	9	AC006534	AC006534 Homo sapi	530	206.6	22.8	255952	2	AL513473	AL513473 Homo sapi

531	206.4	22.8	3621	9	AY204748	604	206.2	22.7	187908	9	HS495010	AL031121	Human DNA
532	206.4	22.8	28420	9	AL162391	605	206.2	22.7	188666	9	AC018921	AC018921	Homo sapi
533	206.4	22.8	35666	9	BX119906	606	206.2	22.7	192618	9	AC092811	AC092811	Homo sapi
534	206.4	22.8	59356	9	AC115109	607	206.2	22.7	200000	9	AP000512	AP000512	Homo sapi
535	206.4	22.8	78415	9	BS000161	608	206.2	22.7	200430	9	AC011500	AC011500	Homo sapi
536	206.4	22.8	96594	6	AK6595647	609	206.2	22.7	201197	2	HS424212	Z82207	Homo sapi
537	206.4	22.8	99594	9	AP263284	610	206.2	22.7	217035	9	AC096669	AC096669	Homo sapi
538	206.4	22.8	104658	9	AP006284	611	206.2	22.7	220007	2	AC148935	AC148935	Homo sapi
539	206.4	22.8	114517	9	AL158152	612	206.2	22.7	339168	2	AC078987	AC078987	Homo sapi
540	206.4	22.8	119951	2	AC025267	613	206	22.7	50564	9	AY338490	AY338490	Homo sapi
541	206.4	22.8	120044	2	AL590116	614	206	22.7	51841	2	AP228703	AP228703	Homo sapi
542	206.4	22.8	145133	2	AC013892	615	206	22.7	52459	9	HSJ735G18	AL118497	Human DNA
543	206.4	22.8	151498	9	AC021739	616	206	22.7	55256	9	HS424212	AL118497	Human DNA
544	206.4	22.8	154813	9	AC131934	617	206	22.7	73029	9	HSB4329J7	AL583856	Human DNA
545	206.4	22.8	155539	9	AL138721	618	206	22.7	79555	9	HS431D10	Z97885	Human DNA
546	206.4	22.8	157242	2	AC083821	619	206	22.7	82517	9	AL604028	AL604028	Human DNA
547	206.4	22.8	159593	2	AC007924	620	206	22.7	97559	9	AL356748	AL356748	Human DNA
548	206.4	22.8	160573	2	AC119676	621	206	22.7	1011720	9	AC005006	AC005006	Homo sapi
549	206.4	22.8	170862	2	AC087784	622	206	22.7	103584	9	AC103959	AC103959	Homo sapi
550	206.4	22.8	171818	9	AC063962	623	206	22.7	109576	2	CR752982	CR752982	Homo sapi
551	206.4	22.8	172963	9	AC134866	624	206	22.7	145327	9	AC114302	AC114302	Homo sapi
552	206.4	22.8	173099	9	AC097501	625	206	22.7	149714	2	AC144499	AC144499	Homo sapi
553	206.4	22.8	183301	2	AC092487	626	206	22.7	151933	2	AC073199	AC055711	Homo sapi
554	206.4	22.8	187294	9	AC084082	627	206	22.7	154850	2	AC055711	AL133336	Homo sapi
555	206.4	22.8	188639	9	AC011236	628	206	22.7	155559	2	HSN14	AP002442	Homo sapi
556	206.4	22.8	194746	2	AC145544	629	206	22.7	156655	2	AP002442	AP002442	Homo sapi
557	206.4	22.8	221636	9	AC006443	630	206	22.7	159620	9	AC009314	AC009314	Homo sapi
558	206.4	22.8	224187	9	AL7732374	631	206	22.7	161788	9	AC021755	AC021755	Homo sapi
559	206.4	22.8	241304	9	AL954220	632	206	22.7	161794	9	AC020687	AC020687	Homo sapi
560	206.4	22.8	250529	9	HUAE000658	633	206	22.7	169571	9	AC012146	AC012146	Homo sapi
561	206.2	22.7	4936	9	AF134406	634	206	22.7	171309	9	AC025168	AC025168	Homo sapi
562	206.2	22.7	21118	9	AF190749	635	206	22.7	173336	9	AC139815	AC139815	Homo sapi
563	206.2	22.7	22038	9	HSBPMF2	636	206	22.7	176277	2	AC139815	AC139815	Homo sapi
564	206.2	22.7	23352	9	AL591166	637	206	22.7	181916	2	AC117181	AC034244	Homo sapi
565	206.2	22.7	39198	6	AX078379	638	206	22.7	182892	9	AC133781	AC133781	Homo sapi
566	206.2	22.7	46610	9	HSU34879	639	206	22.7	185571	9	AC133781	AC133781	Homo sapi
567	206.2	22.7	56270	9	AC117435	640	206	22.7	191414	2	AC144518	AC144518	Homo sapi
568	206.2	22.7	71418	9	AF1732442	641	206	22.7	191764	9	AC009506	AC009506	Homo sapi
569	206.2	22.7	71503	9	AF219991	642	206	22.7	193679	2	AC140510	AC140510	Homo sapi
570	206.2	22.7	75074	9	CR788240	643	206	22.7	193894	9	AC114730	AC114730	Homo sapi
571	206.2	22.7	77908	9	AC008609	644	206	22.7	194516	9	AC024681	AC024681	Homo sapi
572	206.2	22.7	82636	9	AC086728	645	206	22.7	194516	9	AF215848	AF215848	Homo sapi
573	206.2	22.7	86997	2	AC108364	646	206	22.7	199451	2	AC087624	AC087624	Homo sapi
574	206.2	22.7	104755	9	BSX908728	647	206	22.7	206596	2	AC002357	AC002357	Homo sapi
575	206.2	22.7	105104	9	HSJ47817	648	206	22.7	244847	2	AP002357	AP002357	Homo sapi
576	206.2	22.7	110000	2	AL831785.1	649	205.8	22.7	6905	9	HSBPMF4	HSBPMF4	Human thymo
577	206.2	22.7	110000	2	BX294172_0	650	205.8	22.7	35886	9	AC004035	AC004035	Homo sapi
578	206.2	22.7	121212	9	HS135L22	651	205.8	22.7	36428	9	AC005362	AC005362	Homo sapi
579	206.2	22.7	123554	9	AB023049	652	205.8	22.7	44375	9	AC148448	AC148448	Homo sapi
580	206.2	22.7	129252	9	HSU91327	653	205.8	22.7	55588	9	AC073841	AC073841	Homo sapi
581	206.2	22.7	129747	9	HS465N24	654	205.8	22.7	59554	6	AK695587	AK695587	Sequence
582	206.2	22.7	130755	9	AL845353	655	205.8	22.7	74432	9	HS465G10B	HS465G10B	Sequence
583	206.2	22.7	132066	9	AL958382	656	205.8	22.7	84163	9	AL645821	AL645821	Human DNA
584	206.2	22.7	137032	9	AC020982	657	205.8	22.7	97075	9	AC010289	AC010289	Homo sapi
585	206.2	22.7	147102	9	AC002476	658	205.8	22.7	110000	2	BX276116_04	BX276116_04	Continuation (5 of
586	206.2	22.7	149181	2	AL357078	659	205.8	22.7	110525	9	AB020878	AB020878	Homo sapi
587	206.2	22.7	157442	9	AC021813	660	205.8	22.7	114455	9	AL353141	AL353141	Human DNA
588	206.2	22.7	157442	9	AC105001	661	205.8	22.7	118873	9	HS1184P4	HS1184P4	Human DNA
589	206.2	22.7	158608	9	CNS05TDJ	662	205.8	22.7	119631	9	AC008888	AC008888	Homo sapi
590	206.2	22.7	161970	9	AP005660	663	205.8	22.7	130403	9	AL158139	AL158139	Human DNA
591	206.2	22.7	162245	9	AC011008	664	205.8	22.7	137022	9	AC004221	AC004221	Homo sapi
592	206.2	22.7	163444	2	AC025866	665	205.8	22.7	139072	9	AP000485	AP000485	Homo sapi
593	206.2	22.7	164168	9	AL135927	666	205.8	22.7	140176	2	AC016411	AC016411	Homo sapi
594	206.2	22.7	164179	9	AL007227	667	205.8	22.7	143223	2	AL162725	AL162725	Human DNA
595	206.2	22.7	170107	2	AC151445	668	205.8	22.7	146515	2	AC146981	AC146981	Homo sapi
596	206.2	22.7	171467	9	AL448223	669	205.8	22.7	155567	2	AC073492	AC073492	Homo sapi
597	206.2	22.7	171627	9	AL662797	670	205.8	22.7	157813	2	AC015957	AC015957	Homo sapi
598	206.2	22.7	175945	2	AC022147	671	205.8	22.7	158103	9	AC007952	AC007952	Homo sapi
599	206.2	22.7	179146	2	AC067852	672	205.8	22.7	162337	2	AC023999	AC023999	Homo sapi
600	206.2	22.7	179854	2	AC149454	673	205.8	22.7	162943	9	CNS01IDY	CNS01IDY	Human chr
601	206.2	22.7	180347	2	AC009415	674	205.8	22.7	164725	9	AC092938	AC092938	Homo sapi
602	206.2	22.7	184557	2	AC149554	675	205.8	22.7	166857	9	AP005118	AP005118	Homo sapi
603	206.2	22.7	185617	9	AL662848	676	205.8	22.7	168064	2	AC019160	AC019160	Homo sapi

C 677	205.8	22.7	169064	2	AC023767	Homo sapi	C 750	205.6	22.7	193643	9	AC018644	Homo sapi
C 678	205.8	22.7	169979	2	AC013700	Homo sapi	C 751	205.6	22.7	197000	9	AC124859	Homo sapi
C 679	205.8	22.7	171812	9	AC013389	Homo sapi	C 752	205.6	22.7	202815	2	AF267169	Homo sapi
C 680	205.8	22.7	174839	9	AL157395	Human DNA	C 753	205.6	22.7	209859	9	AC084083	Homo sapi
C 681	205.8	22.7	175195	2	AP001319	Homo sapi	C 754	205.6	22.7	209870	9	AC104431	Homo sapi
C 682	205.8	22.7	178236	2	AC060768	Homo sapi	C 755	205.6	22.7	215150	9	AC026689	Homo sapi
C 683	205.8	22.7	178625	2	AC106017	Homo sapi	C 756	205.6	22.7	218074	9	AC023283	Homo sapi
C 684	205.8	22.7	178975	2	AC023222	Homo sapi	C 757	205.6	22.7	218630	2	AC145892	Pan trogl
C 685	205.8	22.7	179272	2	AC069149	Homo sapi	C 758	205.6	22.7	220458	2	AC010320	Homo sapi
C 686	205.8	22.7	179372	2	AC040922	Homo sapi	C 759	205.6	22.7	278310	2	AC069592	Homo sapi
C 687	205.8	22.7	179511	2	AC025283	Homo sapi	C 760	205.4	22.6	2819	6	AX330468	Sequence
C 688	205.8	22.7	179581	2	AC009397	Homo sapi	C 761	205.4	22.6	32638	2	AC146707	Homo sapi
C 689	205.8	22.7	182301	2	AC012498	Homo sapi	C 762	205.4	22.6	41385	9	AC144836	Homo sapi
C 690	205.8	22.7	182431	2	AC068380	Homo sapi	C 763	205.4	22.6	55616	6	BD196412	Prostatic
C 691	205.8	22.7	186115	9	AC008474	Homo sapi	C 764	205.4	22.6	56520	6	BD196564	Prostatic
C 692	205.8	22.7	188100	2	AC134780	Homo sapi	C 765	205.4	22.6	62799	2	AC114687	Homo sapi
C 693	205.8	22.7	188460	2	AC010542	Homo sapi	C 766	205.4	22.6	81403	9	AC092849	Homo sapi
C 694	205.8	22.7	188560	2	AC141415	Pan trogl	C 767	205.4	22.6	95360	2	AC022465	Homo sapi
C 695	205.8	22.7	190025	2	AC140145	Homo sapi	C 768	205.4	22.6	96594	6	AX695779	Sequence
C 696	205.8	22.7	193312	2	AP004370	Homo sapi	C 769	205.4	22.6	96865	2	AC138684	Homo sapi
C 697	205.8	22.7	193390	2	AC013370	Homo sapi	C 770	205.4	22.6	100259	9	AC005800	Homo sapi
C 698	205.8	22.7	194237	2	AC068870	Homo sapi	C 771	205.4	22.6	102202	9	AC027694	Homo sapi
C 699	205.8	22.7	195110	9	AC107943	Homo sapi	C 772	205.4	22.6	104726	9	AC008087	Homo sapi
C 700	205.8	22.7	195913	9	AL954236	Pan trogl	C 773	205.4	22.6	109238	9	AC004997	Homo sapi
C 701	205.8	22.7	198664	9	AP006256	Homo sapi	C 774	205.4	22.6	116470	9	AC099568	Homo sapi
C 702	205.8	22.7	207901	2	AC147043	Pan trogl	C 775	205.4	22.6	118234	9	AL355476	Human DNA
C 703	205.8	22.7	211305	9	AC079988	Homo sapi	C 776	205.4	22.6	126327	9	AC005252	Homo sapi
C 704	205.8	22.7	231490	9	CNS01D03	Human chr	C 777	205.4	22.6	127006	9	AL138849	Human DNA
C 705	205.8	22.7	257967	2	AL365337	Human chr	C 778	205.4	22.6	129293	9	HS1172N10	Human DNA
C 706	205.8	22.7	257967	2	AL365337	Human chr	C 779	205.4	22.6	130282	2	AC1078973	Homo sapi
C 707	205.6	22.7	297235	2	AL499603	Homo sapi	C 780	205.4	22.6	134445	9	AC116648	Homo sapi
C 708	205.6	22.7	401	11	BV190685	BV190685 sqm16804	C 781	205.4	22.6	134471	9	AC005186	Homo sapi
C 709	205.6	22.7	40649	2	AY190788	AY190788 Porco pvg	C 782	205.4	22.6	139376	9	HS095742	Human chrom
C 710	205.6	22.7	45459	2	AC006103	AC003111 Human DNA	C 783	205.4	22.6	142201	9	AC124248	Homo sapi
C 711	205.6	22.7	75237	2	AC022925	AC006103 Homo sapi	C 784	205.4	22.6	143146	9	AC079855	Homo sapi
C 712	205.6	22.7	83969	2	AC005210	AC022925 Homo sapi	C 785	205.4	22.6	150363	2	AL161444	Human DNA
C 713	205.6	22.7	110000	2	AL732359_00	AL732359 Homo sapi	C 786	205.4	22.6	150569	2	AC084228	Homo sapi
C 714	205.6	22.7	110000	2	AL732359_01	Continuation (2 of	C 787	205.4	22.6	155989	9	AL354932	Human DNA
C 715	205.6	22.7	115043	9	AL663070	AL663070 Human DNA	C 788	205.4	22.6	157676	2	AC027358	Homo sapi
C 716	205.6	22.7	118405	9	AC012349	AC012349 Homo sapi	C 789	205.4	22.6	158357	9	AC005585	Homo sapi
C 717	205.6	22.7	131140	2	AC027474	AC027474 Homo sapi	C 790	205.4	22.6	159322	2	AC026085	Homo sapi
C 718	205.6	22.7	131747	9	AC124857	AC124857 Homo sapi	C 791	205.4	22.6	159978	2	AC139479	Homo sapi
C 719	205.6	22.7	134960	2	AP002337	AP002337 Homo sapi	C 792	205.4	22.6	161309	9	AC100839	Homo sapi
C 720	205.6	22.7	137233	2	AC090221	AC090221 Homo sapi	C 793	205.4	22.6	164026	2	AC143349	Homo sapi
C 721	205.6	22.7	141007	2	AC025764	AC025764 Homo sapi	C 794	205.4	22.6	165307	2	AC148831	Pan trogl
C 722	205.6	22.7	142520	2	HS620E11	AL031667 Human DNA	C 795	205.4	22.6	165307	2	AC148831	Pan trogl
C 723	205.6	22.7	151450	9	AC108679	AC108679 Homo sapi	C 796	205.4	22.6	165799	2	AC100813	Homo sapi
C 724	205.6	22.7	151452	2	AP001894	AP001894 Homo sapi	C 797	205.4	22.6	165807	2	AL391810	Homo sapi
C 725	205.6	22.7	152484	2	AC067992	AC067992 Homo sapi	C 798	205.4	22.6	167005	2	AC009822	Homo sapi
C 726	205.6	22.7	153185	2	AC073228	AC073228 Homo sapi	C 799	205.4	22.6	167075	2	AC138885	Homo sapi
C 727	205.6	22.7	155290	9	AL359175	AL359175 Homo sapi	C 800	205.4	22.6	168136	9	AF287957	Homo sapi
C 728	205.6	22.7	160370	9	AC023464	AC023464 Homo sapi	C 801	205.4	22.6	169371	2	AC138902	Homo sapi
C 729	205.6	22.7	170797	9	AC011379	AC011379 Homo sapi	C 802	205.4	22.6	169414	9	AC068707	Homo sapi
C 730	205.6	22.7	170849	9	AC126366	AC126366 Homo sapi	C 803	205.4	22.6	169665	2	AC144566	Homo sapi
C 731	205.6	22.7	172837	2	AL450304	AL450304 Human DNA	C 804	205.4	22.6	170135	2	AC137873	Homo sapi
C 732	205.6	22.7	174856	2	BX296555	BX296555 Homo sapi	C 805	205.4	22.6	172334	2	AC010650	Homo sapi
C 733	205.6	22.7	175050	2	AC027589	AC027589 Homo sapi	C 806	205.4	22.6	172812	9	AC016903	Homo sapi
C 734	205.6	22.7	176278	9	AC024028	AC024028 Homo sapi	C 807	205.4	22.6	172827	9	AC007216	Homo sapi
C 735	205.6	22.7	176550	9	AL356336	AL356336 Human DNA	C 808	205.4	22.6	173525	2	AC067893	Homo sapi
C 736	205.6	22.7	178653	2	AP001591	AP001591 Homo sapi	C 809	205.4	22.6	177483	9	AC068233	Homo sapi
C 737	205.6	22.7	178982	2	AC090088	AC090088 Homo sapi	C 810	205.4	22.6	180221	9	AC007277	Homo sapi
C 738	205.6	22.7	179627	2	AC113426	AC113426 Homo sapi	C 811	205.4	22.6	180392	2	AC192929	Homo sapi
C 739	205.6	22.7	179666	2	AC138145	AC138145 Homo sapi	C 812	205.4	22.6	181277	2	AC139478	Homo sapi
C 740	205.6	22.7	180889	2	AC079986	AC079986 Homo sapi	C 813	205.4	22.6	181597	9	AC090515	Homo sapi
C 741	205.6	22.7	184057	9	AP000753	AP000753 Homo sapi	C 814	205.4	22.6	182092	9	AC013477	Homo sapi
C 742	205.6	22.7	184059	2	AC090382	AC090382 Homo sapi	C 815	205.4	22.6	183107	9	AC096539	Homo sapi
C 743	205.6	22.7	184512	9	AC079804	AC079804 Homo sapi	C 816	205.4	22.6	183485	2	AC022578	Homo sapi
C 744	205.6	22.7	184840	9	AC079907	AC079907 Homo sapi	C 817	205.4	22.6	183861	9	AC078816	Homo sapi
C 745	205.6	22.7	184886	9	AC005358	AC005358 Homo sapi	C 818	205.4	22.6	184148	2	AC148725	Homo sapi
C 746	205.6	22.7	184889	9	AL442125	AL442125 Human DNA	C 819	205.4	22.6	184585	9	AC079465	Homo sapi
C 747	205.6	22.7	185242	2	AC084709	AC084709 Homo sapi	C 820	205.4	22.6	184649	2	AC025185	Homo sapi
C 748	205.6	22.7	191291	2	AC148313	Pan trogl	C 821	205.4	22.6	185182	9	AC093423	Homo sapi
C 749	205.6	22.7	192203	9	AC034102	AC034102 Homo sapi	C 822	205.4	22.6	185834	2	AC009632	Homo sapi

823	205.4	22.6	185964	9	AC009399	AC009399 Homo sapi	896	205	22.6	84678	2	AC087464	AC087464 Homo sapi
824	205.4	22.6	186212	2	AC006938	AC006938 Homo sapi	897	205	22.6	88018	9	AC010418	AC010418 Homo sapi
825	205.4	22.6	189579	9	AL1354733	Human DNA	898	205	22.6	90096	9	AL611925	AL611925 Human DNA
826	205.4	22.6	190483	2	AC148839	AC148839 Pan trogl	899	205	22.6	91224	9	AC093582	AC093582 Homo sapi
827	205.4	22.6	191729	2	AL590872	AL590872 Homo sapi	900	205	22.6	94166	9	AL133415	AL133415 Human DNA
828	205.4	22.6	192126	9	DJ7270M14	DJ7270M14 Homo sapi	901	205	22.6	94635	9	AC139931	AC139931 Homo sapi
829	205.4	22.6	196337	9	AL1358975	AL1358975 Human DNA	902	205	22.6	95855	9	HSAC000115	AC000115 Homo sapi
830	205.4	22.6	196421	2	AC090780	AC090780 Homo sapi	903	205	22.6	98876	9	AC009488	AC009488 Homo sapi
831	205.4	22.6	199079	2	AC097267	AC097267 Pan trogl	904	205	22.6	105787	9	AC113367	AC113367 Homo sapi
832	205.4	22.6	199230	2	AC048360	AC048360 Homo sapi	905	205	22.6	107642	9	AC093859	AC093859 Homo sapi
833	205.4	22.6	199454	2	AC117180	AC117180 Homo sapi	906	205	22.6	109761	9	AF271405	AF271405 Homo sapi
834	205.4	22.6	202768	2	AC092345	AC092345 Homo sapi	907	205	22.6	112351	9	AC001484	AC001484 Homo sapi
835	205.4	22.6	204963	2	AC145617	AC145617 Homo sapi	908	205	22.6	115888	9	AC002468	AC002468 Homo sapi
836	205.4	22.6	206737	2	AC126917	AC126917 Homo sapi	909	205	22.6	112417	9	AC006015	AC006015 Homo sapi
837	205.4	22.6	209718	2	AC091099	AC091099 Homo sapi	910	205	22.6	123004	9	HS1097F14	HS1097F14 Human DNA
838	205.4	22.6	210688	2	AC137498	AC137498 Homo sapi	911	205	22.6	123657	9	AL139125	AL139125 Human DNA
839	205.4	22.6	210867	2	AC144878	AC144878 Pongo pyg	912	205	22.6	124437	9	AL135914	AL135914 Human DNA
840	205.4	22.6	213481	9	AC134618	AC134618 Homo sapi	913	205	22.6	125495	9	HS510D11	HS510D11 Human DNA
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842	205.4	22.6	225116	9	AC134619	AC134619 Homo sapi	915	205	22.6	132414	2	AL1359882	AL1359882 Homo sapi
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844	205.4	22.6	231234	2	AL591116	AL591116 Homo sapi	917	205	22.6	133154	9	HSBDJ90K10	HSBDJ90K10 Human DNA
845	205.4	22.6	237952	2	AL591116	AL591116 Homo sapi	918	205	22.6	135894	9	AC145425	AC145425 Homo sapi
846	205.4	22.6	248344	2	AC134883	AC134883 Homo sapi	919	205	22.6	144859	9	AC104997	AC104997 Homo sapi
847	205.4	22.6	328187	2	AC117393	AC117393 Homo sapi	920	205	22.6	145201	9	AC084854	AC084854 Homo sapi
848	205.2	22.6	301	6	AX741028	Sequence	921	205	22.6	146551	9	AC112249	AC112249 Homo sapi
849	205.2	22.6	3674	9	AF517523	AF517523 Homo sapi	922	205	22.6	147999	2	AL161635	AL161635 Homo sapi
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853	205.2	22.6	88215	9	AC006963	AC006963 Homo sapi	926	205	22.6	155382	2	AC127520	AC127520 Homo sapi
854	205.2	22.6	95240	9	AC026718	AC026718 Homo sapi	927	205	22.6	156551	2	HS537K23	HS537K23 Homo sapi
855	205.2	22.6	111321	2	AC026718	AC026718 Homo sapi	928	205	22.6	157515	2	AL1391598	AL1391598 Homo sapi
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857	205.2	22.6	120825	9	AC0110465	AC0110465 Homo sapi	930	205	22.6	160133	2	AC024355	AC024355 Homo sapi
858	205.2	22.6	123221	9	AC011472	AC011472 Homo sapi	931	205	22.6	160878	2	AC016971	AC016971 Homo sapi
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861	205.2	22.6	129169	2	AC032038	AC032038 Homo sapi	934	205	22.6	162840	2	AC063917	AC063917 Homo sapi
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864	205.2	22.6	143790	2	AC055811	AC055811 Homo sapi	937	205	22.6	168922	9	CNS01DPT	AL133778 Human chr
865	205.2	22.6	153223	2	AC074339	AC074339 Homo sapi	938	205	22.6	170125	9	AC024082	AC024082 Homo sapi
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872	205.2	22.6	172876	9	AC114489	AC114489 Homo sapi	945	205	22.6	186291	9	AC145984	AC145984 Pan trogl
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874	205.2	22.6	173977	9	AC010170	AC010170 Homo sapi	947	205	22.6	188295	9	AC122133	AC122133 Homo sapi
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876	205.2	22.6	174559	9	AC015720	AC015720 Homo sapi	949	205	22.6	191103	9	AC025271	AC025271 Homo sapi
877	205.2	22.6	174724	2	AC140096	AC140096 Pan trogl	950	205	22.6	191330	9	AC065271	AC065271 Homo sapi
878	205.2	22.6	178902	2	AL513525	AL513525 Homo sapi	951	205	22.6	191433	9	AF053356	AF053356 Homo sapi
879	205.2	22.6	178985	9	HS340B19	HS340B19 Human DNA	952	205	22.6	227968	9	AF205588	AF205588 Homo sapi
880	205.2	22.6	179221	9	AC114493	AC114493 Homo sapi	953	205	22.6	312283	9	HS2W06	HS2W06 Human chr
881	205.2	22.6	185167	9	AC009777	AC009777 Homo sapi	954	204.8	22.6	3234	9	AF205588	AF205588 Homo sapi
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883	205.2	22.6	191594	9	AC009851	AC009851 Homo sapi	956	204.8	22.6	46894	9	AC114729	AC114729 Homo sapi
884	205.2	22.6	194156	2	AP002954	AP002954 Homo sapi	957	204.8	22.6	68003	2	EX322853	EX322853 Homo sapi
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886	205.2	22.6	198410	2	AP000831	AP000831 Homo sapi	959	204.8	22.6	69912	2	AC010322	AC010322 Homo sapi
887	205.2	22.6	199321	2	AP000941	AP000941 Homo sapi	960	204.8	22.6	100130	9	AC090454	AC090454 Homo sapi
888	205.2	22.6	204001	2	AC073640	AC073640 Homo sapi	961	204.8	22.6	102387	9	AC022114	AC022114 Homo sapi
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890	205.2	22.6	204769	2	AC150377	AC150377 Homo sapi	963	204.8	22.6	108316	2	AX647597	AX647597 Sequence
891	205.2	22.6	213025	2	AC021159	AC021159 Homo sapi	964	204.8	22.6	110000	6	AL1390202	AL1390202 Homo sapi
892	205.2	22.6	242913	9	AL1732409	AL1732409 Homo sapi	965	204.8	22.6	116506	9	AL161613	AL161613 Homo sapi
893	205	22.6	16765	9	AL733409	AL733409 Human DNA	966	204.8	22.6	122292	9	AY029472	AY029472 Homo sapi
894	205	22.6	48832	9	HS301K23	HS301K23 Human DNA	967	204.8	22.6	126080	9	AY029472	AY029472 Homo sapi
895	205	22.6	82251	9	AC004506	AC004506 Homo sapi	968	204.8	22.6	127399	9	AL158825	AL158825 Human DNA

969	204.8	22.6	135311	9	AC008798	Homo sapi	1042	204.6	22.6	173618	2	AC019045	Homo sapi
970	204.8	22.6	135618	2	AL359965	Homo sapi	c1043	204.6	22.6	174387	9	AC092350	Homo sapi
c 971	204.8	22.6	136002	9	AL3120024	Homo sapi	1044	204.6	22.6	177180	9	AC092350	Homo sapi
c 972	204.8	22.6	142273	9	AL3120024	Homo sapi	1045	204.6	22.6	177607	2	AC027272	Homo sapi
c 973	204.8	22.6	147514	9	AC008521	Homo sapi	c1046	204.6	22.6	183894	9	AC040970	Homo sapi
c 974	204.8	22.6	155452	9	AL049646	Homo sapi	c1047	204.6	22.6	191824	9	AL161935	Homo sapi
c 975	204.8	22.6	159791	9	HS056829	Homo sapi	1048	204.6	22.6	192409	2	AC072033	Homo sapi
976	204.8	22.6	160850	9	AC009951	Homo sapi	1049	204.6	22.6	192898	9	AC145968	Homo sapi
c 977	204.8	22.6	165920	9	AC010222	Homo sapi	c1050	204.6	22.6	197630	9	AC011676	Homo sapi
c 978	204.8	22.6	168727	9	AC118658	Homo sapi	1051	204.6	22.6	197752	2	AC145130	Homo sapi
c 979	204.8	22.6	168931	2	AC144998	Homo sapi	c1052	204.6	22.6	198470	9	AC046170	Homo sapi
c 980	204.8	22.6	169193	2	AC068523	Homo sapi	1053	204.6	22.6	198564	9	AC008581	Homo sapi
c 981	204.8	22.6	169908	2	AC150910	Homo sapi	c1054	204.6	22.6	200420	9	AC138645	Homo sapi
c 982	204.8	22.6	170423	9	AC018663	Homo sapi	1055	204.6	22.6	200594	9	AC093117	Homo sapi
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c 984	204.8	22.6	174902	2	AC110071	Homo sapi	c1057	204.6	22.6	203790	9	AC010422	Homo sapi
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c 986	204.8	22.6	176526	9	AP005230	Homo sapi	c1059	204.6	22.6	210949	2	AC146885	Homo sapi
c 987	204.8	22.6	177750	9	AC005874	Homo sapi	1060	204.6	22.6	212426	9	AC104335	Homo sapi
c 988	204.8	22.6	177864	9	AP134471	Homo sapi	1061	204.6	22.6	220173	9	AC012183	Homo sapi
c 989	204.8	22.6	177978	9	AC009073	Homo sapi	c1062	204.6	22.6	221484	2	AC144877	Homo sapi
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c 991	204.8	22.6	181923	9	AC022872	Homo sapi	1064	204.6	22.6	226696	9	AC139026	Homo sapi
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c 994	204.8	22.6	186953	9	AC025678	Homo sapi	1067	204.6	22.6	281662	2	AC117374	Homo sapi
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c1000	204.8	22.6	215422	9	U66060	Homo sapi	c1073	204.4	22.5	11954	9	AL133275	Homo sapi
c1001	204.8	22.6	230552	9	AC005098	Homo sapi	c1074	204.4	22.5	16242	9	AL136091	Homo sapi
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c1003	204.6	22.6	26096	9	AL160055	Homo sapi	c1076	204.4	22.5	33550	9	AC003004	Homo sapi
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c1005	204.6	22.6	41026	9	AC131159	Homo sapi	1078	204.4	22.5	61233	9	AL1662859	Homo sapi
c1006	204.6	22.6	68774	9	AY430083	Homo sapi	1079	204.4	22.5	67581	2	AC027802	Homo sapi
c1007	204.6	22.6	80878	9	AC114480	Homo sapi	1080	204.4	22.5	90103	2	CR788295	Homo sapi
c1008	204.6	22.6	85763	9	AL359455	Homo sapi	1081	204.4	22.5	92058	9	BX119924	Homo sapi
c1009	204.6	22.6	1005190	9	AC061992	Homo sapi	c1082	204.4	22.5	93634	2	AC127088	Homo sapi
c1010	204.6	22.6	102517	2	AP002876	Homo sapi	1083	204.4	22.5	99249	9	AL161916	Homo sapi
c1011	204.6	22.6	1103875	9	AL136223	Homo sapi	1084	204.4	22.5	100562	9	AL355870	Homo sapi
c1012	204.6	22.6	11074	9	AC007569	Homo sapi	1085	204.4	22.5	102479	9	AC115107	Homo sapi
c1013	204.6	22.6	112351	9	AC011484	Homo sapi	1086	204.4	22.5	103158	9	AL1662871	Homo sapi
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c1015	204.6	22.6	114340	9	AL358232	Homo sapi	1088	204.4	22.5	106928	9	AC005049	Homo sapi
c1016	204.6	22.6	116451	9	AL355860	Homo sapi	c1089	204.4	22.5	106954	9	AC104651	Homo sapi
c1017	204.6	22.6	122764	9	HS0831D17	Homo sapi	1090	204.4	22.5	107526	9	HS111M5	Homo sapi
c1018	204.6	22.6	125579	9	AL161772	Homo sapi	1091	204.4	22.5	108048	9	AC115108	Homo sapi
c1019	204.6	22.6	129441	9	AL136170	Homo sapi	1092	204.4	22.5	111651	9	CR626938	Homo sapi
c1020	204.6	22.6	140800	2	AC018392	Homo sapi	c1093	204.4	22.5	112453	6	CR689788	Homo sapi
c1021	204.6	22.6	145190	2	AC008730	Homo sapi	c1094	204.4	22.5	112973	9	CR847517	Homo sapi
c1022	204.6	22.6	148131	9	AC109489	Homo sapi	1095	204.4	22.5	117051	9	AC115106	Homo sapi
c1023	204.6	22.6	148285	2	AL451053	Homo sapi	1096	204.4	22.5	118338	9	AC010463	Homo sapi
c1024	204.6	22.6	150714	2	AC090278	Homo sapi	1097	204.4	22.5	127761	9	AC006014	Homo sapi
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c1027	204.6	22.6	154158	2	AL365257	Homo sapi	c1100	204.4	22.5	134793	9	AC020922	Homo sapi
c1028	204.6	22.6	158617	9	AC135972	Homo sapi	1101	204.4	22.5	147833	2	AC087486	Homo sapi
c1029	204.6	22.6	159597	9	AC008747	Homo sapi	c1102	204.4	22.5	147885	2	AL353793	Homo sapi
c1030	204.6	22.6	159989	2	AC138687	Homo sapi	1103	204.4	22.5	154251	2	AC116974	Homo sapi
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c1035	204.6	22.6	166553	2	AL844523	Homo sapi	1108	204.4	22.5	160426	2	AL353805	Homo sapi
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c1038	204.6	22.6	167110	2	AC022621	Homo sapi	c1111	204.4	22.5	162445	2	AC022488	Homo sapi
c1039	204.6	22.6	168268	9	AC009124	Homo sapi	c1112	204.4	22.5	163126	9	AC110012	Homo sapi
c1040	204.6	22.6	170705	9	AC034459	Homo sapi	1113	204.4	22.5	165382	2	AC024408	Homo sapi
c1041	204.6	22.6	171477	9	AC026457	Homo sapi	1114	204.4	22.5	167286	2	AP001638	Homo sapi

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1116	204.4	22.5	169059	2	AC009790	Homo sapi	c1189	204.2	22.5	123160	9	AL153719	AL153719 Human DNA
c1117	204.4	22.5	169439	9	AC008021	Homo sapi	1190	204.2	22.5	129203	9	AC104819	AC104819 Homo sapi
c1118	204.4	22.5	169825	9	AC012652	Homo sapi	1191	204.2	22.5	129608	9	AL153685	AL153685 Human DNA
c1119	204.4	22.5	170655	2	AP001012	Homo sapi	1192	204.2	22.5	132521	9	AC008710	AC008710 Homo sapi
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c1123	204.4	22.5	175872	9	AP001266	Homo sapi	1196	204.2	22.5	135964	9	AC005914	AC005914 Homo sapi
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c1126	204.4	22.5	178029	9	AC106037	Homo sapi	c1199	204.2	22.5	143969	9	AL157552	AL157552 Human DNA
c1127	204.4	22.5	178066	9	AC106037	Homo sapi	1200	204.2	22.5	144695	2	AC012438	AC012438 Homo sapi
c1128	204.4	22.5	178828	9	AL1357507	Human DNA	1201	204.2	22.5	145253	9	AC006329	AC006329 Homo sapi
c1129	204.4	22.5	182230	9	AC135050	Homo sapi	c1202	204.2	22.5	149034	9	AP275948	AP275948 Homo sapi
c1130	204.4	22.5	182320	9	AC135050	Homo sapi	c1203	204.2	22.5	149249	9	AC079945	AC079945 Homo sapi
1131	204.4	22.5	183085	9	AC005815	Homo sapi	c1204	204.2	22.5	149370	9	AC012626	AC012626 Homo sapi
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c1133	204.4	22.5	185779	9	AC091231	Homo sapi	1206	204.2	22.5	151228	9	AL662800	AL662800 Human DNA
c1134	204.4	22.5	188640	2	AC146153	Homo sapi	1207	204.2	22.5	152556	9	CNS01DSY	AL122035 Human chr
c1135	204.4	22.5	193212	9	AP004370	Homo sapi	c1208	204.2	22.5	152714	9	BS000156	BS000156 Pan trogl
c1136	204.4	22.5	194189	2	AC103705	Homo sapi	c1209	204.2	22.5	153609	9	HSAPJ9617	AJ009617 Homo sapi
c1137	204.4	22.5	195476	2	AC135044	Homo sapi	c1210	204.2	22.5	153609	9	AC006557	AC006557 Homo sapi
c1138	204.4	22.5	195834	9	AC105418	Homo sapi	1211	204.2	22.5	155800	2	AC146667	AC146667 Homo sapi
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c1140	204.4	22.5	197807	2	AC147057	Homo sapi	c1213	204.2	22.5	156264	9	AC103921	AC103921 Homo sapi
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c1142	204.4	22.5	201844	9	CNS05STCL	Human chr	1215	204.2	22.5	158103	9	AC007952	AC007952 Homo sapi
c1143	204.4	22.5	203050	2	HS44N10	Homo sapi	c1216	204.2	22.5	160012	2	AL136231	AL136231 Human DNA
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1145	204.4	22.5	210608	9	AC006028	Homo sapi	1218	204.2	22.5	162948	9	AL662822	AL662822 Human DNA
c1146	204.4	22.5	212237	9	AC079235	Homo sapi	c1219	204.2	22.5	164282	2	AC015734	AC015734 Homo sapi
c1147	204.4	22.5	212336	2	AC147650	Homo sapi	1220	204.2	22.5	164958	9	AC099340	AC099340 Homo sapi
c1148	204.4	22.5	214866	9	AC069544	Homo sapi	1221	204.2	22.5	165227	9	AC025884	AC025884 Homo sapi
c1149	204.4	22.5	224770	2	AC061712	Homo sapi	1222	204.2	22.5	168210	9	AC018719	AC018719 Homo sapi
1150	204.4	22.5	235313	2	AC148034	Homo sapi	1223	204.2	22.5	169460	9	AC104370	AC104370 Homo sapi
c1151	204.2	22.5	601	11	BV196817	Seqm19048	1224	204.2	22.5	170048	2	AC025240	AC025240 Homo sapi
1152	204.2	22.5	2748	9	AC004124	Homo sapi	c1225	204.2	22.5	170686	9	AC012595	AC012595 Homo sapi
c1153	204.2	22.5	4646	6	AX127798	Sequence	1226	204.2	22.5	170797	9	AC011379	AC011379 Homo sapi
c1154	204.2	22.5	4646	6	AX127798	Sequence	1227	204.2	22.5	170803	2	AC016155	AC016155 Homo sapi
c1155	204.2	22.5	4736	6	AR393493	Sequence	1228	204.2	22.5	170908	2	AC022557	AC022557 Homo sapi
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1162	204.2	22.5	39000	9	AC002322	Homo sapi	1235	204.2	22.5	180155	2	AC026556	AC026556 Homo sapi
1163	204.2	22.5	39634	2	AC139315	Homo sapi	1236	204.2	22.5	182454	9	AP001004	AP001004 Homo sapi
c1165	204.2	22.5	40948	9	AC140106	Homo sapi	c1237	204.2	22.5	183689	2	AC146129	AC146129 Pan trogl
c1166	204.2	22.5	43600	9	AC004209	Homo sapi	1238	204.2	22.5	183854	2	AC145951	AC145951 Homo sapi
1167	204.2	22.5	44983	2	AC139093	Homo sapi	c1239	204.2	22.5	183999	6	AX092589	AX092589 Sequence
1168	204.2	22.5	59078	9	AL606807	Homo sapi	1240	204.2	22.5	184302	9	AL162393	AL162393 Human DNA
1169	204.2	22.5	60563	2	AC137682	Homo sapi	c1241	204.2	22.5	185463	9	AC016065	AC016065 Homo sapi
1170	204.2	22.5	64172	9	BX000357	Human DNA	1242	204.2	22.5	186210	9	AC007596	AC007596 Homo sapi
1171	204.2	22.5	70448	9	CR388372	Human DNA	c1243	204.2	22.5	187461	9	AL550453	AL550453 Homo sapi
1172	204.2	22.5	73641	2	CR758912	Homo sapi	1244	204.2	22.5	188863	9	AC068769	AC068769 Homo sapi
c1173	204.2	22.5	81195	9	AL627143	Human DNA	1245	204.2	22.5	191246	9	AC084420	AC084420 Homo sapi
c1174	204.2	22.5	82724	9	BX927220	Human DNA	1246	204.2	22.5	191292	2	AC129804	AC129804 Homo sapi
c1175	204.2	22.5	92029	2	AL357934	Human DNA	1247	204.2	22.5	192450	2	AC147313	AC147313 Pan trogl
1176	204.2	22.5	95505	9	AL357934	Human DNA	c1248	204.2	22.5	192853	9	AC040173	AC040173 Homo sapi
c1177	204.2	22.5	100000	9	AP000514	Homo sapi	c1249	204.2	22.5	192971	2	AL550708	AL550708 Human DNA
1178	204.2	22.5	102105	9	AL136166	Human DNA	c1250	204.2	22.5	194056	9	AL550708	AL550708 Human DNA
c1179	204.2	22.5	107506	9	HS0472M2	Human DNA	c1251	204.2	22.5	194173	9	CNS01RGM	AL160231 Human chr
1180	204.2	22.5	110000	2	AC117731	Continuation (2 of	1252	204.2	22.5	196037	9	AC129492	AC129492 Homo sapi
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1182	204.2	22.5	113066	2	AC026729	Homo sapi	1254	204.2	22.5	199882	9	AF287262	AF287262 Homo sapi
c1183	204.2	22.5	113906	2	AC136589	Homo sapi	c1255	204.2	22.5	201144	2	HS424J12	HS424J12 Homo sapi
c1184	204.2	22.5	115793	9	AC104115	Homo sapi	c1256	204.2	22.5	201397	2	AC136933	AC136933 Homo sapi
1185	204.2	22.5	118504	9	AC094080	Homo sapi	c1257	204.2	22.5	203330	2	AC145989	AC145989 Pan trogl
1186	204.2	22.5	119847	9	AF064866	Homo sapi	c1258	204.2	22.5	204393	2	AC145989	AC145989 Pan trogl
1187	204.2	22.5	121930	2	CR762481	Homo sapi	c1259	204.2	22.5	205498	9	AF079416	AF079416 Homo sapi
							c1260	204.2	22.5	213611	9	AF276759	AF276759 Homo sapi

1261	204.2	22.5	228516	9	AC002523	Homo sapi	1334	204	22.5	198316	2	AC019157	Homo sapi
c1262	204.2	22.5	238637	2	AC112167	Homo sapi	1335	204	22.5	200771	2	AC133587	Homo sapi
1263	204.2	22.5	286224	2	AC115881	Pen trogl	1336	204	22.5	201886	2	AC092700	Homo sapi
1264	204.2	22.5	340000	9	HS21C083	Homo sapi	c1337	204	22.5	202983	2	AC024249	Homo sapi
c1265	204	22.5	22845	9	HSJA09943	Homo sapi	c1338	204	22.5	210675	2	AC026272	Homo sapi
c1266	204	22.5	33137	6	AX646721	Sequence	1339	204	22.5	237931	9	AC022098	Homo sapi
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c1268	204	22.5	35327	9	AP227509	Homo sapi	c1341	203.8	22.5	3237	9	HMS17DC57Z	Homo sapi
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c1271	204	22.5	59012	9	HSABLRG2	Human DNA	c1344	203.8	22.5	8735	6	CQ797971	Sequence
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c1273	204	22.5	68843	9	HSJ654417	Human DNA	c1346	203.8	22.5	8735	6	AF242195	Homo sapi
c1274	204	22.5	70346	9	AL161614	Human DNA	1347	203.8	22.5	14411	2	AL592152	Human DNA
1275	204	22.5	71120	2	AC124800	Homo sapi	c1348	203.8	22.5	39596	9	AL445257	Homo sapi
c1276	204	22.5	90241	2	AC006974	Homo sapi	1349	203.8	22.5	39915	9	AC010512	Homo sapi
1277	204	22.5	90877	9	AC069436	Homo sapi	c1350	203.8	22.5	41055	9	AC006930	Homo sapi
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1279	204	22.5	95018	9	ALJ392107	Human DNA	1352	203.8	22.5	51932	9	AC114275	Homo sapi
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1281	204	22.5	105596	9	ALJ39223	Human DNA	c1354	203.8	22.5	57070	9	AL354721	Human DNA
c1282	204	22.5	106526	9	AF042089	Homo sapi	c1355	203.8	22.5	57729	9	AL449284	Human DNA
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1285	204	22.5	113998	9	AC011509	Human DNA	c1358	203.8	22.5	67853	9	AL844175	Human DNA
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1288	204	22.5	116102	2	AC131236	Homo sapi	c1361	203.8	22.5	77436	2	AC004581	Homo sapi
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1290	204	22.5	120335	9	HSJ441A12	Human DNA	c1363	203.8	22.5	84207	9	AC092471	Homo sapi
1291	204	22.5	123149	9	AC008655	Homo sapi	c1364	203.8	22.5	98778	2	AC002408	Homo sapi
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c1293	204	22.5	124441	2	AC027098	Homo sapi	c1366	203.8	22.5	103273	9	AC139932	Homo sapi
1294	204	22.5	129695	9	AC127035	Homo sapi	c1367	203.8	22.5	109238	9	AC004997	Homo sapi
1295	204	22.5	131708	9	ALJ354710	Human DNA	c1368	203.8	22.5	110000	2	BR293554_0	Homo sapi
c1297	204	22.5	132923	9	AC115097	Homo sapi	1369	203.8	22.5	111873	9	AC073275	Homo sapi
1296	204	22.5	136959	9	AC092115	Homo sapi	c1370	203.8	22.5	113911	9	AC093685	Homo sapi
c1298	204	22.5	137074	9	AF130248	Homo sapi	1371	203.8	22.5	114793	9	AP000769	Homo sapi
1299	204	22.5	148336	9	AC007710	Homo sapi	c1372	203.8	22.5	117628	9	AC008891	Homo sapi
c1300	204	22.5	149461	9	AC139453	Homo sapi	c1373	203.8	22.5	120416	9	AC093915	Homo sapi
c1301	204	22.5	150332	9	AC004921	Homo sapi	1374	203.8	22.5	122228	9	AC004773	Homo sapi
c1302	204	22.5	153863	2	AC025361	Homo sapi	c1375	203.8	22.5	126995	9	AC004703	Homo sapi
1303	204	22.5	156601	9	HS212G6	Human DNA	c1376	203.8	22.5	128312	9	AL591885	Human DNA
c1304	204	22.5	156678	2	AC149449	Pen trogl	c1377	203.8	22.5	129462	9	AL391056	Human DNA
1305	204	22.5	164813	9	AC025154	Homo sapi	c1378	203.8	22.5	131933	9	AL590311	Human DNA
1306	204	22.5	165187	9	AP003716	Homo sapi	1379	203.8	22.5	131943	9	AC005484	Homo sapi
1307	204	22.5	165733	2	AC069072	Homo sapi	c1380	203.8	22.5	132457	9	AC016584	Homo sapi
c1308	204	22.5	166288	2	ALJ39410	Human DNA	c1381	203.8	22.5	134457	9	AC001231	Homo sapi
c1309	204	22.5	166532	2	AC022279	Homo sapi	1382	203.8	22.5	142664	9	ALJ36985	Human DNA
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1312	204	22.5	171004	2	AC006286	Homo sapi	1385	203.8	22.5	147052	9	AL590640	Human DNA
c1313	204	22.5	171914	2	AF246928	Homo sapi	c1386	203.8	22.5	147401	2	AC067778	Homo sapi
1314	204	22.5	173808	2	AC036206	Homo sapi	c1387	203.8	22.5	147854	9	AC021422	Homo sapi
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c1317	204	22.5	177028	9	AC025043	Homo sapi	c1390	203.8	22.5	155824	2	AC087296	Homo sapi
c1318	204	22.5	178050	9	AC142324	Pen trogl	1391	203.8	22.5	156461	9	AC004383	Homo sapi
1319	204	22.5	180531	9	AC008745	Homo sapi	c1392	203.8	22.5	157248	9	AC002312	Human Chr
c1320	204	22.5	182295	2	AP001501	Homo sapi	c1393	203.8	22.5	157620	9	BS000109	Pen trogl
1321	204	22.5	183097	2	AC027638	Homo sapi	c1394	203.8	22.5	157750	9	AL512599	Human DNA
c1322	204	22.5	183773	9	AC087284	Homo sapi	c1395	203.8	22.5	158257	9	AC005585	Homo sapi
1323	204	22.5	185916	2	AP001558	Homo sapi	1396	203.8	22.5	158338	2	AC024720	Homo sapi
c1324	204	22.5	187516	2	AC009648	Homo sapi	c1397	203.8	22.5	159506	9	HS3416	Human DNA
1325	204	22.5	188453	9	AC025521	Homo sapi	c1398	203.8	22.5	159976	2	AC016124	Homo sapi
c1326	204	22.5	188812	9	ALJ357055	Human DNA	1399	203.8	22.5	160604	9	AC008608	Homo sapi
1327	204	22.5	19631	2	AC011842	Homo sapi	1400	203.8	22.5	160672	9	AC009048	Homo sapi
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1329	204	22.5	190306	9	AC146080	Pen trogl	1402	203.8	22.5	166439	2	AC025342	Homo sapi
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c1331	204	22.5	191236	9	AC090519	Homo sapi	c1404	203.8	22.5	168528	9	ALJ35861	Human DNA
1332	204	22.5	193509	2	AC026868	Homo sapi	c1405	203.8	22.5	169313	9	AP001782	Homo sapi
1333	204	22.5	196170	2	AC087527	Homo sapi	1406	203.8	22.5	169599	2	AC026041	Homo sapi

1407	203.8	22.5	170823	2	AC133549	Homo sapi	1480	203.6	22.4	173271	2	AC141623	Homo sapi
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1411	203.8	22.5	173910	9	AC083982	Homo sapi	1484	203.6	22.4	174428	2	AC136441	Homo sapi
1412	203.8	22.5	178733	2	AC068786	Homo sapi	1485	203.6	22.4	174539	2	AC103558	Homo sapi
1413	203.8	22.5	178877	2	AC093311	Homo sapi	1486	203.6	22.4	175053	2	AC023226	Homo sapi
1414	203.8	22.5	179236	2	AC005143	Homo sapi	1487	203.6	22.4	175095	2	AC140895	Homo sapi
1415	203.8	22.5	181489	9	AC104828	Homo sapi	1488	203.6	22.4	175785	2	AC138897	Homo sapi
1416	203.8	22.5	182892	9	AC034244	Homo sapi	1489	203.6	22.4	175786	2	AC105339	Homo sapi
1417	203.8	22.5	184311	2	AC120517	Pan trogl	1490	203.6	22.4	176630	2	AC010684	Homo sapi
1418	203.8	22.5	185147	2	AC147193	Papio anu	1491	203.6	22.4	176713	9	AP000751	Homo sapi
1419	203.8	22.5	192440	9	CNS01DXH	Human chr	1492	203.6	22.4	176927	2	AC127469	Papio anu
1420	203.8	22.5	197019	9	AL157938	Human DNA	1493	203.6	22.4	177470	9	AL357140	Human DNA
1421	203.8	22.5	199522	9	AC089999	Homo sapi	1494	203.6	22.4	178710	9	AC011477	Homo sapi
1422	203.8	22.5	209421	9	AC090543	Homo sapi	1495	203.6	22.4	179048	9	AC096642	Homo sapi
1423	203.8	22.5	211025	2	AL1590875	Homo sapi	1496	203.6	22.4	180664	2	AC140896	Homo sapi
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1438	203.6	22.4	46967	2	AC107930	Homo sapi	AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.					
1439	203.6	22.4	60268	9	AC016876	Homo sapi	TITLE	Implant, method of making same and use of the implant for the					
1440	203.6	22.4	60461	9	AF245699	Homo sapi	JOURNAL	Patent: US 6478825-A 398 12-NOV-2002;					
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DEFINITION Sequence 97 from Patent WO0193983.
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VERSION     AX358844.1  GI:18675323
KEYWORDS
SOURCE      Homo sapiens (human)
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REFERENCE   1
            Baker K.P., Deeneyers,L., Gerritsen,M.E., Goddard A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
            Secreted and transmembrane polypeptides and nucleic acids encoding
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            Patent: WO 0193983-A 97 13-DEC-2001;
JOURNAL     Genentech Inc. (US)
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Query Match      100.0%; Score 907; DB 6; Length 907;
Best Local Similarity 100.0%; Pred. No. 1e-244;
Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 97 from Patent WO0208288.
ACCESSION  AX362337
VERSION     AX362337.1  GI:18694626
KEYWORDS
SOURCE      Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerlitsen, M.E., Goddard, A.,
Gadowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 97 31-JAN-2002;
Genentech, Inc. (US)
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Query Match 100.0%; Score 907; DB 6; Length 907;
Best Local Similarity 100.0%; Pred. No. 1e-244;
Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION AX403511.1 GI:21436996
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,
Ferrara, N., Gerber, H., Gerlitsen, M., Goddard, A., Gadowski, P.,
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
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QY	661 TGGAGGCCGAGGCGGGTGGATCACTGAGATCAGAGATTCAAGACCAAGCCTTGGCCAACA	720
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QY	841 TGCGGTAGGCCGAGATCGCGCGCTGATTTCCAGCTTGGCGACAAAGTGAAGCTTCATC	900
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Db	17953 TCACACA 17947	

RESULT 7	
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LOCUS	AC067930
DEFINITION	Homo sapiens chromosome 8, clone RP11-661A12, complete sequence.
ACCESSION	AC067930
VERSION	AC067930.7
KEYWORDS	GI:21954034
SOURCE	HTG.
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Best Local Similarity 100.0%; Pred. No. 1.1e-244; Indels 0; Gaps 0;

Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGACTGTGAGGCTCCAGACGCTGTCTGAGGCCCCCAAGAGAGTGTTCACCTTGAC 60
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QY 61 CCTAGGGGCTGGATTGTCTGTTAAACAAGATTAAGGAGGAGCCCACTAGGGA 120
DB 126354 CCTAGGGGCTGGATTGTCTGTTAAACAAGATTAAGGAGGAGCCCACTAGGGA 126295
QY 121 ATGCTACTCTCTGCTCCCTCCAGCTGCGGTGTTCACGGTGCCTGTCCTCTTGCC 180
DB 126294 ATGCTACTCTCTGCTCCCTCCAGCTGCGGTGTTCACGGTGCCTGTCCTCTTGCC 126235
QY 181 GAGAGAGTGTCTGGGTCAAGGAGCGAGAGAGCGCTCAAGACTCCAGCCCTTGTATCC 240
DB 126234 GAGAGAGTGTCTGGGTCAAGGAGCGAGAGAGCGCTCAAGACTCCAGCCCTTGTATCC 126175
QY 241 GAGAGAGCACTTGGCAGAGTCCAGAGTGTCTGGAGTCCACACAGACTGGCGGCAAG 300
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QY 301 GCAGAGGGGAGCAGTTCTGTGTGTGTGTGAGCAGTAAGAGGCTCTTGCCAGTCCA 360
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QY 361 GGGTGGGGGGCGGCAAACTTCATAAAGAACAGAGGCTTGGGCCCGGCACAGAGTCA 420
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QY 421 TCTGGCCAGCTCTCTGCTGCTGCGGAGGAGTGGGAGTGGGAGTGGGCTTGTGTCAG 480
DB 125994 TCTGGCCAGCTCTCTGCTGCTGCGGAGGAGTGGGAGTGGGAGTGGGCTTGTGTCAG 125935
QY 481 TAAACCAAGCTGAGTTGCTGCGGCGCAATGTCTCTGTCTAGGAGCAATCTCA 540
DB 125934 TAAACCAAGCTGAGTTGCTGCGGCGCAATGTCTCTGTCTAGGAGCAATCTCA 125875
QY 541 ACCTTCTGCTCTCAGAGACCCCAAGAGCTTCAATTGATCTATTGATTTTACACATT 600
DB 125874 ACCTTCTGCTCTCAGAGACCCCAAGAGCTTCAATTGATCTATTGATTTTACACATT 125815
QY 601 AGCAATTAACCTGAGAAATGGGCGGAGCGGAGTGGCTCAGCGCTGTATCCAGACATT 660
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QY 661 TGGAGGCGGAGCGGAGTGCATCAGTGAATCAGAGTTCAGAACCAAGCTGGCCACA 720
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QY 841 TGGGATGAGCCGAGATCGCGCGCTGATTCAGAGCTGGGCGCAAGAGTGAAGATTCATC 900
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QY 901 TCACACA 907
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RESULT 8
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LOCUS Homo sapiens chromosome 8 clone RP11-545C16, WORKING DRAFT
DEFINITION
AC019122
SEQUENCE, 12 unordered pieces.
AC019122 3 GI:8318560
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 207636)
REFERENCE
AUTHORS Waterston,R.H.
TITLES The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 207636)
TITLES Waterston,R.H.
JOURNAL Direct Submission
SUBMITTED (30-DEC-1999) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 7, 2000 this sequence version replaced gi:7109639.

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----- Project Information -----
Center project name: H_NH0545C16
----- Summary Statistics -----
Sequencing vector: M13; 88%
Sequencing vector: Plasmid; 12%
Chemistry: Dye-primed ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198432 bases at least Q40
Consensus quality: 201424 bases at least Q30
Consensus quality: 203070 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 206536; sum-of-contigs
Quality coverage: 6.36 in Q20 bases; agarose-fp
Quality coverage: 5.66 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1654 1753: gap of unknown length
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* 1754 3687: contig of 1934 bp in length
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* 3688 3787: gap of unknown length
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* 3788 11012: contig of 7225 bp in length
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* 11013 11112: gap of unknown length
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* 11113 16540: contig of 5428 bp in length
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* 16541 16640: gap of unknown length
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* 16641 23739: contig of 7099 bp in length
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* 23740 23839: gap of unknown length
*
* 23840 35039: contig of 11200 bp in length
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* 35040 35139: gap of unknown length
*
* 35140 54231: contig of 19092 bp in length
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* 54232 54331: gap of unknown length
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* 54332 78481: contig of 24050 bp in length
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* 78482 78481: gap of unknown length
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* 78482 106509: contig of 28028 bp in length
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* 106510 106509: gap of unknown length
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* 106510 130451: contig of 23842 bp in length
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* 130452 130551: gap of unknown length
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* 130552 157163: contig of 26612 bp in length
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	Matches 907;	Conservative	0;	Mismatches	0;	
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QY	61	CCCTAAGGAGTCTGAGATTGCTGTTAAACAAGTAACTGAGGAGCAGACCCGANTAGGGA	120			
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QY	721	TGGTGAACCTTGTCTAATAAATAACAAAAATTAGCCAGGCAAGTGTGTGCACTGG	780			
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QY	781	TAGTCCCAAGTTACTCGGAGAGGCTGAGGCAAGAAATCGCTGAACCAAGAGGCGGACGT	840			
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OY      901 TCACACA 907
Db      88896 TCACACA 88902

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DEFINITION Homo sapiens chromosome 8 clone RP11-545C16 map 8, *** SEQUENCING
IN PROGRESS ***
ACCESSION AC087823
VERSION   AC087823.2
KEYWORDS  HTG; HTGS PHASE1.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Birren,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE     1 (bases 1 to 164959)
JOURNAL   Homo sapiens chromosome 8, clone RP11-545C16
REFERENCE
AUTHORS  2 (bases 1 to 164959)
TITLE     Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bascien,V., Boguslavsky,L., Bouhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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McPheters,R., Meidirim,J., Meneus,J., Mihova,T., Menga,V.,
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O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunhahng,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Sancio,R., Schauer,S., Schupack,R., Seaman,S., Severy,P.,
Soutuez,C., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Sudamanian,A., Talamas,J., Testaye,S., Theodore,J.,
Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Vtel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
COMMENT  Submitted (28-JAN-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 16, 2001 this sequence version replaced gi:12584321.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11736
Center clone name: 545_C16

* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Best Local Similarity 100.0%; Pred. No. 2e-242;
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Qy 69 GTCTGAGATTGCTGTTAAACAAGTAACCTGAGGCGAGAGCCCATAGGGGAATGCTACC 128
Db 41682 GTCTGAGATTGCTGTTAAACAAGTAACCTGAGGCGAGAGCCCATAGGGGAATGCTACC 41623

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Qy 129 TCTTGCCCTTCCACCTGCCCCCTGGTGTTCACGGTGGCTGGTCCCTTGGCCGAGAGAT 188
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Db 41502 ACTTGGCAAGTTCAGAGATGCTCCGAGTCCACACACAGACTGGGCGGAGGCGAGAGAG 41443
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Qy 369 GGGGGAACCTCCATTAAGAACAGAGGGTCTGGGCCCCGCGCCACAGAGTCAATCTGCCA 428
Db 41382 GGGGGAACCTCCATTAAGAACAGAGGGTCTGGGCCCCGCGCCACAGAGTCAATCTGCCA 41323
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Db 41142 AAACGAGAAATGGCCGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 41083
Qy 669 CGAGCGGGTGTGATCACTGATCACTGATCACTGATCACTGATCACTGATCACTGATCA 728
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Qy 789 GTTACTCGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 848
Db 40962 GTTACTCGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 40903
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Db 40902 GCCGAGATCGCGCGCTGATTCAGGCTTGAACCCAGAGGCGGAGCTTGGCGGTGA 40844

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RESULT 10
ARI29215 500 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 73 from patent US 6183968.
DEFINITION ARI29215
ACCESSION ARI29215
VERSION ARI29215.1 GI:14116877
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 500)
Bandman, O., Lal, P., Hillman, J.L., Yue, H., Reddy, R., Guejter, K.J.,
and Baughn, M.R.
Composition for the detection of genes encoding receptors and
proteins associated with cell proliferation
Patent: US 6183968-A 73 06-FBB-2001;
JOURNAL Location/Qualifiers
FEATURES
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/organism="unknown"

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ORIGIN /mol_type="unassigned DNA"

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DB 1 TTCCACTGCTCCCTGCTTTCAGAGTGGCCCTGCTCCCTTCCGAGAGATTCCTGGG 60

QY 197 TCAGGACGACGAGAGAGCTCAGAGACTCAGGCTTTTGTATCCGAGAGACACTTGGCA 256
DB 61 TCAGGACGACGAGAGAGCTCAGAGACTCAGGCTTTTGTATCCGAGAGACACTTGGCA 120

QY 257 AGGTCCAGCGATGCTCCGAGTCCACACAGACTGGCGGACAGAGGGGAGACAGT 316
DB 121 AGGTCCAGCGATGCTCCGAGTCCACACAGACTGGCGGACAGAGGGGAGACAGT 180

QY 317 TCTGTTGCTTGGTTCAGATTAAGGCTTTGGCACTCCAGGTTGGGGGGCGGCA 376
DB 181 TCTGTTGCTTGGTTCAGATTAAGGCTTTGGCACTCCAGGTTGGGGGGCGGCA 240

QY 377 ACTCCATAAAGACAGAGGCTTGGGCCCGGACAGAGTATGCTCCAGCTCCTT 436
DB 241 ACTCCATAAAGACAGAGGCTTGGGCCCGGACAGAGTATGCTCCAGCTCCTT 300

QY 437 GCTGCTGGCAGTGGAGTGGCAAGAGTGGGGCTTTGTGCGAGTAAACACAGGCTGG 496
DB 301 GCTGCTGGCAGTGGAGTGGCAAGAGTGGGGCTTTGTGCGAGTAAACACAGGCTGG 360

QY 497 ATTGGCTGGGGGCAATGCTCTGTCTAGGAGCAATTCATCCTTTTCTCTCAG 556
DB 361 ATTGGCTGGGGGCAATGCTCTGTCTAGGAGCAATTCATCCTTTTCTCTCAG 420

QY 557 GACCCCAAAGACTTCAATGTATCTATTTTACCATTTAGCAATTTAAACTGAG 616
DB 421 GACCCCAAAGACTTCAATGTATCTATTTTACCATTTAGCAATTTAAACTGAG 480

QY 617 AAATGGCGCGGACCGGTGG 636
DB 481 AAATGGCGCGGACCGGTGG 500

RESULT 11
CQ462746/c 480 bp DNA linear PAT 30-JAN-2004
LOCUS CQ462746
DEFINITION Sequence 5524 from Patent WO0192581.
ACCESSION CQ462746
VERSION CQ462746.1 GI:41428365
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Algate, P.A., Harlocker, S.L. and Jones, R.
Compositions and methods for the therapy and diagnosis of
ovarian cancer
Patent: WO 0192581-A 5524 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
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DB 480 ATAGGGGAATGTACTCTGCTCCCTTCACCTGCGCTGTGTTACAGGTGGCTGGTCCC 421

QY 173 TCCTTCCGACAGAGAGTGTCTTGCTCAGGAGCAGAGAGACGCTCAGACTCCAGCCCT 232
DB 420 TCCTTCCGACAGAGAGTGTCTTGCTCAGGAGCAGAGAGACGCTCAGACTCCAGCCCT 361

QY 233 TTGTTACCGAGAGGACACTTGGCAAGGTCCAGGATGTGCTGGAGTCCACACAGACTG 292
DB 360 TTGTTACCGAGAGGACACTTGGCAAGGTCCAGGATGTGCTGGAGTCCACACAGACTG 301

QY 293 GCGGACGAGCAGAGAGGAGCAGTTCTGTTGTCTTGTGAGACATTAAGAGGCTTGG 352
DB 300 GCGGACGAGCAGAGAGGAGCAGTTCTGTTGTCTTGTGAGACATTAAGAGGCTTGG 241

QY 353 CCAATCCAGGAGTGGGGGGGCGCAACTCCATTAAGAACAGAGGCTTGGGCCCGGCA 412
DB 240 CCAATCCAGGAGTGGGGGGGCGCAACTCCATTAAGAACAGAGGCTTGGGCCCGGCA 182

QY 413 CAGAGTCACTGCGCCAGCTCTGCTGCTGGCCAGTGGAGATGGCAGAGGTTGGGCTT 472
DB 181 CAGAGTCACTGCGCCAGCTCTGCTGCTGGCCAGTGGAGATGGCAGAGGTTGGGCTT 122

QY 473 TGTGCAAGTAAACACAGAGCTGGAATTTGCTGCGGGCCATGATCTCTAGGCGAC 532
DB 121 TGTGCAAGTAAACACAGAGCTGGAATTTGCTGCGGGCCATGATCTCTAGGCGAC 63

QY 533 AATTCGAACCTTCTTGTCTCTCAGAGCCCAAGACTTCAATGTATCTAATTTT 592
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DB 2 AC 1

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LOCUS CQ460389
DEFINITION Sequence 3167 from Patent WO0192581.
ACCESSION CQ460389
VERSION CQ460389.1 GI:41426008
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Algate, P.A., Harlocker, S.L. and Jones, R.
Compositions and methods for the therapy and diagnosis of
ovarian cancer
Patent: WO 0192581-A 3167 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1. 425
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ORIGIN

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QY 228 GCCCTTTTGAACGAGAGACACTTGGCAAGGTCCAGAGCATGTCCGGAGTCCACACACA 287
DB 365 GCCCTTTTGAACGAGAGACACTTGGCAAGGTCCAGAGCATGTCCGGAGTCCACACACA 306

QY 288 GACTGGCGGACAGGAGCAGAGGGGAGACAGTTCTGTTGTGCTTGGTGAAGTGAAGAGGT 347

Db 305 GACTGCGGAGGCGAGGAGGAGGACGTTCTGTGTGCTTGTGACAGTAAGAGGT 246
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Db 245 CTTCGCGAGTCAGGGGTGGGGGGGCGCAATCCATTAAGAACAGAGGCTT-GGCCCC 187
Qy 408 GCGCACAGAGTCATCTGCCCCAGCTCTCTGTGTGCGCAAGTGGAGTCACAGAGTGG 467
Db 186 GGCACAGAGTCATCTGCCCCAGGCTCTCTGTGTGCGCAAGTGGAGTCACAGAGTGG 127
Qy 468 GGCCTTGTGCGCAATTAAGACAGAGGCTGTGATTTGCTCGGGCCATAGTCTCTTAA 527
Db 126 GGCCTTGTGCGCAATTAAGACAGAGGCTGTGATTTG-CTGCGGGCCATAGTCTCTTAA 68
Qy 528 GCAGCAATTCACCTTCTGTGCTCTAGAGACCCCAAGAGCTTCAATGTATCTATTGA 587
Db 67 GCAGCAATTCACCTTCTGTGCTCTAGAGACCCCAAGAGCTTCAATGTATCTATTGA 8
Qy 588 TTTTAC 594
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RESULT 13
LOCUS CQ460821 402 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 3599 from Patent WO0192581.
ACCESSION CQ460821
VERSION CQ460821.1 GI:41426440
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Algate,P.A., Harlocker,S.L. and Jones,R.
Compositions and methods for the therapy and diagnosis of
ovariencancer
Patent: WO 0192581-A 3599 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
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Location/Qualifiers
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Db 342 CTTCGCAAGGTCAGGAGTGTCCGAGTCCACACAGACTGCGGCGGAGGAGAGG 283
Qy 310 GGAAGTTCGTGTGTGTGTGTGAGACGTAAAGGGTCTTGGCGAGTCAAGGTTGGGG 369
Db 282 GGAAGTTCGTGTGTGTGTGTGAGACGTAAAGGGTCTTGGCGAGTCAAGGTTGGGG 223
Qy 370 GCGGCAATCTCATTAAGAACAGAGGCTTGGGCGGCGGCGGCGGAGTCTTGGCCAG 429
Db 222 GCGGCAATCTCATTAAGAACAGAGGCTTGGGCGGCGGCGGCGGAGTCTTGGCCAG 164
Qy 430 CTCCTGT 489
Db 163 CTCCTGT 104
Qy 490 AGGCTGATTTGCTGCGGGGCAATGATCCTGTCTAAGGGGACGAAATTCCTTCTTG 549

Db 103 AGGCTGATTTG-CTGCGGGCCAT-GTCCGTCTAAGGACAGAAATTCCTTCTTG 46
Qy 550 CTTCAGAGACCCCAAGAGCTTCAATGTATCTAATTTTAC 594
Db 45 CTTCAGAGACCCCAAGAGCTTCAATGTATCTAATTTTAC 1
RESULT 14
LOCUS CQ463335 360 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 6113 from Patent WO0192581.
ACCESSION CQ463335
VERSION CQ463335.1 GI:41428954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Algate,P.A., Harlocker,S.L. and Jones,R.
Compositions and methods for the therapy and diagnosis of
ovariencancer
Patent: WO 0192581-A 6113 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
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Best Local Similarity 98.9%; Pred.No. 6.4e-86;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Qy 294 CCGCAGGGCAGAGGGGAGCAGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 353
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Qy 474 GTGCAAGTAAACACAGAGGTCGATTTGCTGCGGGGCGGCGGCGGCGGCGGCGGCGG 533
Db 121 GTGCAAGTAAACACAGAGGTCGATTTGCTGCGGGGCGGCGGCGGCGGCGGCGGCGG 62
Qy 534 ATTCTCAACCTTCTGTCTCAGAGCCCAAGAGCTTCAATGTATCTAATTTTAA 593
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Qy 594 C 594
Db 1 C 1
RESULT 15
LOCUS AX071596 399 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 2068 from Patent WO0102568.
ACCESSION AX071596
VERSION AX071596.1 GI:12581947
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Williams,L.T., Escobedo,J., Inliss,M.A., Garcia,P.D., Klinger,J.,
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamsom,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leskowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
Human genes and gene expression products
Patent: WO 0102568-A 2068 11-JAN-2001;
CHIRON CORPORATION (US) ; HYSEQ, INC. (US)

TITLE
JOURNAL

FEATURES
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ORIGIN

Query Match 24.6%; Score 222.8; DB 6; Length 399;
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Matches 224; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 234 CCTTAGGGGCTGTGGATTGTGTGTTAACAGATTAACCTTGAGGGCAGAGACCCCATAGGGGA 293
Qy 121 ATGCTACCTCTGCTGCCCTTCCACCTGCGCTGTGTTCAAGGTGAGCTGTGTCCTCTTGCC 180
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Db 354 GAGAGAGTGTCTGTGGTCAAGGAGCGCAGAGAGAGCTCACAGACTCC 399

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OM nucleic - nucleic search, using sw model

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SUMMARIES

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179	907	100.0	907	Sequence 1596, App
180	601.6	66.3	1154	Sequence 204, App
C 181	458	50.5	480	Sequence 5524, App
C 182	403	44.4	425	Sequence 3167, App

C 183	369	40.7	402	9	US-09-867-701-3599	Sequence 3599, App
C 184	344.2	37.9	360	9	US-09-867-701-6113	Sequence 6113, App
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188	212.8	23.5	32148	10	US-09-764-891-6906	Sequence 6906, App
189	212.2	23.4	17397	9	US-09-764-869-1945	Sequence 1945, App
190	212.2	23.4	17397	14	US-10-091-504-1945	Sequence 1945, App
191	212.2	23.4	17397	17	US-10-227-577-1945	Sequence 1945, App
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196	212.2	23.4	19345	17	US-10-227-577-1944	Sequence 1944, App
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C 199	211.8	23.4	177587	13	US-10-087-192-1438	Sequence 1438, App
C 200	211.6	23.3	118931	13	US-10-087-192-1438	Sequence 1438, App
C 201	211.2	23.3	24664	9	US-09-764-887-613	Sequence 613, App
C 202	211.2	23.3	24664	14	US-10-073-961-613	Sequence 613, App
C 203	210.6	23.2	126990	19	US-10-717-597-68	Sequence 68, App
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205	209.6	23.1	28316	22	US-10-893-315-165	Sequence 165, App
206	209.6	23.1	28316	22	US-10-893-315-166	Sequence 166, App
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210	209.4	23.1	152744	22	US-10-981-277-41	Sequence 41, App
211	209.4	23.1	153191	22	US-10-981-277-40	Sequence 40, App
212	209.4	23.1	181279	22	US-10-981-277-38	Sequence 38, App
213	209.2	23.1	614	10	US-09-764-891-9433	Sequence 9433, App
214	209.2	23.1	614	17	US-10-091-414-101	Sequence 301, App
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217	209.2	23.1	691	13	US-10-027-632-110237	Sequence 110237, App
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222	209.2	23.1	16225	17	US-10-091-414-300	Sequence 300, App
C 223	209.2	23.1	50000	10	US-09-902-214-6	Sequence 6, App
C 224	209.2	23.1	59065	16	US-10-135-696-3	Sequence 3, App
C 225	209.2	23.1	59065	19	US-10-820-220-3	Sequence 3, App
226	209.2	23.1	128988	19	US-10-775-169-345	Sequence 345, App
C 227	209	23.0	122673	22	US-10-737-082-35	Sequence 33, App
C 228	209	23.0	122673	22	US-10-765-790-33	Sequence 33, App
C 229	209	23.0	330926	20	US-10-719-993-7048	Sequence 7048, App
C 230	209	23.0	439892	13	US-10-087-192-454	Sequence 454, App
231	208.8	23.0	28253	22	US-10-893-315-152	Sequence 152, App
232	208.8	23.0	28253	22	US-10-893-315-153	Sequence 153, App
233	208.8	23.0	43712	20	US-10-723-860-1576	Sequence 1576, App
C 234	208.8	23.0	119036	21	US-10-723-860-15721	Sequence 17721, App
235	208.6	23.0	518	9	US-09-764-847-1799	Sequence 1799, App
236	208.6	23.0	518	14	US-10-092-154-1799	Sequence 1799, App
237	208.6	23.0	167163	17	US-10-394-948-31	Sequence 31, App
C 238	208.2	23.0	171843	22	US-10-981-277-44	Sequence 44, App
C 239	208	22.9	291	9	US-09-964-824-509	Sequence 509, App
240	208	22.9	291	9	US-09-969-347-1	Sequence 1, App
241	208	22.9	291	9	US-10-843-641A-5812	Sequence 5812, App
242	208	22.9	291	21	US-10-843-641A-6130	Sequence 6130, App
C 243	207.8	22.9	473	19	US-10-674-124A-19604	Sequence 19604, App
C 244	207.8	22.9	166181	20	US-10-723-860-1452	Sequence 1452, App
C 245	207.8	22.9	166181	20	US-10-723-860-1452	Sequence 1452, App
C 246	207.6	22.9	31766	9	US-09-765-344-5	Sequence 3281, App
C 247	207.6	22.9	31766	14	US-10-288-478-5	Sequence 5, App
C 248	207.6	22.9	73764	19	US-10-741-601-5616	Sequence 5616, App
C 249	207.6	22.9	93011	20	US-10-719-993-6871	Sequence 6871, App
C 250	207.2	22.8	403035	19	US-10-322-696-70	Sequence 70, App
C 251	206.8	22.8	169639	19	US-10-322-696-70	Sequence 70, App
C 252	206.4	22.8	96594	11	US-09-997-732-11	Sequence 22, App
C 253	206.2	22.7	603	13	US-10-027-623-151880	Sequence 191880, App
C 254	206.2	22.7	603	17	US-10-027-623-151880	Sequence 191880, App
C 255	206.2	22.7	34096	13	US-10-087-192-952	Sequence 952, App

C 256	206.2	22.7	48436	9	US-09-927-602-38	Sequence 38, Appl	C 329	204	22.5	33137	17	US-10-232-798-913	Sequence 913, App
C 257	206	22.7	113486	20	US-10-417-1375-18	Sequence 18, Appl	C 330	204	22.5	48841	10	US-09-844-653-32	Sequence 32, Appl
C 258	205.8	22.7	13948	13	US-10-087-109-46	Sequence 46, Appl	C 331	204	22.5	81924	19	US-10-741-601-8636	Sequence 5636, Ap
C 259	205.8	22.7	59554	18	US-10-052-482-202	Sequence 202, App	C 332	203.8	22.5	717	13	US-10-027-632-130796	Sequence 130796,
C 260	205.8	22.7	203654	9	US-09-820-905-3	Sequence 3, Appl1	C 333	203.8	22.5	717	13	US-10-027-632-130796	Sequence 130796,
C 261	205.8	22.7	203654	22	US-10-473-338A-3	Sequence 3, Appl1	C 334	203.8	22.5	892	17	US-10-027-632-164445	Sequence 164445,
C 262	205.8	22.7	260549	21	US-10-741-600-17723	Sequence 17723, A	C 335	203.8	22.5	892	17	US-10-027-632-164445	Sequence 164445,
C 263	205.6	22.7	10085	10	US-09-764-891-5491	Sequence 5491, Ap	C 336	203.8	22.5	8735	18	US-10-344-394-13	Sequence 13, Appl
C 264	205.6	22.7	142519	22	US-10-479-874A-9	Sequence 9, Appl1	C 337	203.8	22.5	8735	18	US-10-344-394-13	Sequence 13, Appl
C 265	205.4	22.6	710	13	US-10-027-633-110510	Sequence 110510,	C 338	203.8	22.5	16640	21	US-10-741-600-17666	Sequence 17666, Ap
C 266	205.4	22.6	710	17	US-10-027-633-110510	Sequence 110510,	C 339	203.8	22.5	16640	21	US-10-741-601-5717	Sequence 17617, A
C 267	205.4	22.6	860	13	US-10-027-633-130797	Sequence 130797,	C 340	203.8	22.5	18335	19	US-10-741-600-17851	Sequence 17851, A
C 268	205.4	22.6	860	17	US-10-027-633-130797	Sequence 130797,	C 341	203.8	22.5	18335	19	US-10-052-482-220	Sequence 220, App
C 269	205.4	22.6	2619	19	US-10-363-829-250	Sequence 250, App	C 342	203.8	22.5	60461	17	US-10-341-434-82	Sequence 82, Appl
C 270	205.4	22.6	56516	9	US-09-901-484A-1	Sequence 1, Appl1	C 343	203.6	22.4	56461	17	US-10-341-434-82	Sequence 82, Appl
C 271	205.4	22.6	56516	9	US-09-853-526-1	Sequence 1, Appl1	C 344	203.4	22.4	888	13	US-10-027-632-121467	Sequence 121467,
C 272	205.4	22.6	56520	9	US-09-901-484A-179	Sequence 179, App	C 345	203.4	22.4	888	17	US-10-027-632-121467	Sequence 121467,
C 273	205.4	22.6	56520	9	US-09-853-526-179	Sequence 179, App	C 346	203.4	22.4	4067	10	US-09-764-891-7222	Sequence 7225, Ap
C 274	205.4	22.6	67253	22	US-10-737-082-88	Sequence 88, Appl	C 347	203.4	22.4	4067	10	US-09-764-891-7225	Sequence 338, App
C 275	205.4	22.6	67253	22	US-10-765-790-88	Sequence 88, Appl	C 348	203.4	22.4	32190	14	US-10-073-961-138	Sequence 17, Appl
C 276	205.4	22.6	96594	11	US-09-997-722-154	Sequence 154, App	C 349	203.4	22.4	32190	14	US-10-073-961-138	Sequence 17, Appl
C 277	205.4	22.6	150535	22	US-10-981-277-36	Sequence 36, Appl	C 350	203.4	22.4	56737	9	US-09-782-378A-17	Sequence 17, Appl
C 278	205.4	22.6	166536	22	US-10-981-277-35	Sequence 35, Appl	C 351	203.4	22.4	191395	18	US-10-235-132A-45	Sequence 45, Appl
C 279	205.2	22.6	301	15	US-10-255-434-2	Sequence 2, Appl1	C 352	203.4	22.4	238417	21	US-10-461-862-98	Sequence 98, Appl
C 280	205.2	22.6	1098	13	US-10-027-633-10720	Sequence 10720, A	C 353	203.2	22.4	194883	13	US-10-087-192-826	Sequence 826, App
C 281	205.2	22.6	1098	17	US-10-514-744-42	Sequence 10720, A	C 354	203.2	22.4	256190	19	US-10-322-281-320	Sequence 320, App
C 282	205.2	22.6	3660	22	US-10-514-744-3	Sequence 42, Appl	C 355	203	22.4	718	13	US-10-027-632-102137	Sequence 102137,
C 283	205.2	22.6	3673	22	US-10-514-744-3	Sequence 3, Appl1	C 356	203	22.4	718	13	US-10-027-632-102138	Sequence 102138,
C 284	205.2	22.6	3673	22	US-10-514-744-9	Sequence 9, Appl1	C 357	203	22.4	718	17	US-10-027-632-102138	Sequence 102138,
C 285	205.2	22.6	3674	22	US-10-514-744-1	Sequence 1, Appl1	C 358	203	22.4	718	17	US-10-027-632-102138	Sequence 102138,
C 286	205.2	22.6	3674	22	US-10-514-744-11	Sequence 11, Appl1	C 359	203	22.4	99014	9	US-09-880-107-3428	Sequence 3428, Ap
C 287	205.2	22.6	3675	22	US-10-514-744-7	Sequence 7, Appl1	C 360	203	22.4	114793	5	US-10-148-806-3	Sequence 3, Appl1
C 288	205.2	22.6	3702	21	US-10-514-744-5	Sequence 5, Appl1	C 361	203	22.4	114793	5	US-10-148-806-3	Sequence 3, Appl1
C 289	205.2	22.6	14558	21	US-10-741-600-1569	Sequence 1569, A	C 362	203	22.4	193074	22	US-10-859-792-3	Sequence 3, Appl1
C 290	205.2	22.6	17138	21	US-10-741-600-18009	Sequence 18009, A	C 363	203	22.4	193074	22	US-10-859-792-3	Sequence 43, Appl
C 291	205.2	22.6	18303	17	US-10-741-600-17807	Sequence 17807, A	C 364	203	22.4	1790242	20	US-10-719-893-7640	Sequence 640, Ap
C 292	205.2	22.6	51001	21	US-10-189-268-11	Sequence 11, Appl	C 365	202.8	22.4	3753	13	US-09-764-891-6924	Sequence 7624, Ap
C 293	205	22.6	227968	14	US-10-723-870-1357	Sequence 1357, Ap	C 366	202.8	22.4	14448	17	US-09-860-670-250	Sequence 250, App
C 294	204.8	22.6	289	20	US-10-115-278-3	Sequence 3, Appl1	C 367	202.8	22.4	14448	17	US-10-227-646-250	Sequence 253, App
C 295	204.8	22.6	289	20	US-10-762-966-3	Sequence 3, Appl1	C 368	202.8	22.4	14451	9	US-09-860-670-253	Sequence 253, App
C 296	204.8	22.6	51001	17	US-10-189-268-11	Sequence 11, Appl	C 369	202.8	22.4	14451	17	US-10-227-646-253	Sequence 6605, App
C 297	204.8	22.6	108316	17	US-10-292-798-1789	Sequence 1789, Ap	C 370	202.8	22.4	22259	10	US-09-764-891-6605	Sequence 469, App
C 298	204.8	22.6	108317	15	US-10-017-161-2143	Sequence 2143, App	C 371	202.8	22.4	22259	14	US-10-091-572-169	Sequence 5, Appl1
C 299	204.8	22.6	168749	17	US-10-085-117-250	Sequence 250, App	C 372	202.8	22.4	27067	19	US-09-841-158-5	Sequence 5, Appl1
C 300	204.8	22.6	684973	9	US-09-263-959-1	Sequence 1, Appl1	C 373	202.8	22.4	27067	19	US-10-801-837-5	Sequence 338, App
C 301	204.6	22.6	96589	13	US-10-085-117-130	Sequence 130, App	C 374	202.8	22.4	99886	13	US-10-087-192-328	Sequence 146, App
C 302	204.6	22.6	122614	17	US-10-087-192-1726	Sequence 1726, Ap	C 375	202.8	22.4	101885	20	US-10-723-860-146	Sequence 1810, Ap
C 303	204.6	22.6	247682	18	US-10-235-192A-28	Sequence 28, Appl	C 376	202.8	22.4	133532	13	US-10-087-192-1810	Sequence 18699, Ap
C 304	204.4	22.5	14417	9	US-09-860-670-251	Sequence 251, App	C 377	202.6	22.3	702	13	US-10-027-632-136699	Sequence 136699,
C 305	204.4	22.5	14417	9	US-09-860-670-251	Sequence 249, App	C 378	202.6	22.3	702	17	US-10-027-632-136699	Sequence 1, Appl1
C 306	204.4	22.5	14426	17	US-10-227-646-249	Sequence 249, App	C 379	202.6	22.3	3353	9	US-09-963-159-1	Sequence 1605, Ap
C 307	204.4	22.5	14426	17	US-10-227-646-249	Sequence 17954, A	C 380	202.6	22.3	3353	18	US-10-423-543-43	Sequence 38, Appl
C 308	204.4	22.5	20538	21	US-10-741-600-17954	Sequence 17954, A	C 381	202.6	22.3	3360	17	US-10-311-034-38	Sequence 639, App
C 309	204.4	22.5	23597	21	US-10-741-600-17628	Sequence 17628, A	C 382	202.6	22.3	3343	20	US-10-370-715B-639	Sequence 2427, Ap
C 310	204.4	22.5	167163	17	US-10-394-948-31	Sequence 31, Appl	C 383	202.6	22.3	20669	14	US-10-091-504-42427	Sequence 2427, Ap
C 311	204.4	22.5	4736	17	US-10-452-510-15	Sequence 15, Appl	C 384	202.6	22.3	20669	14	US-10-091-504-42427	Sequence 2427, Ap
C 312	204.2	22.5	4736	18	US-10-617-134-15	Sequence 15, Appl	C 385	202.6	22.3	20669	17	US-10-227-577-2427	Sequence 2427, Ap
C 313	204.2	22.5	4736	19	US-10-744-465-15	Sequence 15, Appl	C 386	202.4	22.3	585	13	US-10-027-632-273703	Sequence 273703,
C 314	204.2	22.5	4736	19	US-10-833-679-15	Sequence 15, Appl	C 387	202.4	22.3	585	17	US-10-027-632-273703	Sequence 273703,
C 315	204.2	22.5	4736	22	US-10-818-279-15	Sequence 15, Appl	C 388	202.4	22.3	795	13	US-10-027-632-171351	Sequence 171351,
C 316	204.2	22.5	11754	10	US-09-984-827-5	Sequence 5, Appl1	C 389	202.4	22.3	795	17	US-10-027-632-171351	Sequence 171351,
C 317	204.2	22.5	83712	19	US-10-741-601-5705	Sequence 5705, Ap	C 390	202.4	22.3	32195	9	US-09-764-870-611	Sequence 611, App
C 318	204.2	22.5	83712	21	US-10-741-600-17805	Sequence 17805, A	C 391	202.4	22.3	32195	9	US-09-764-870-611	Sequence 611, App
C 319	204.2	22.5	155572	22	US-10-981-277-30	Sequence 30, Appl	C 392	202.4	22.3	32195	9	US-09-764-869-1605	Sequence 1605, Ap
C 320	204.2	22.5	159138	20	US-10-719-993-6777	Sequence 6777, Ap	C 393	202.4	22.3	32195	11	US-09-764-875-1513	Sequence 1233, Ap
C 321	204.2	22.5	159138	21	US-10-741-600-16777	Sequence 16773, A	C 394	202.4	22.3	32195	14	US-10-125-540-611	Sequence 617, App
C 322	204.2	22.5	183999	19	US-10-745-377-1	Sequence 1, Appl1	C 395	202.4	22.3	32195	14	US-10-125-540-611	Sequence 1605, Ap
C 323	204.2	22.5	183999	20	US-10-745-377-1	Sequence 1, Appl1	C 396	202.4	22.3	32195	17	US-10-091-504-1505	Sequence 1605, Ap
C 324	204	22.5	691	13	US-10-027-633-263957	Sequence 263957,	C 397	202.4	22.3	32195	17	US-10-227-577-1505	Sequence 1576, Ap
C 325	204	22.5	691	13	US-10-027-633-263957	Sequence 263957,	C 398	202.4	22.3	43712	19	US-10-723-860-15765	Sequence 1576, Ap
C 326	204	22.5	820	17	US-10-027-633-25801	Sequence 25801, A	C 399	202.4	22.3	59942	20	US-10-741-601-5775	Sequence 5775, Ap
C 327	204	22.5	820	17	US-10-027-633-25801	Sequence 25801, A	C 400	202.4	22.3	129381	21	US-10-461-862-28	Sequence 28, Appl
C 328	204	22.5	22927	10	US-09-764-891-7470	Sequence 7470, Ap	C 401	202.2	22.3	850	13	US-10-027-632-30982	Sequence 30982, A

548	200.8	22.1	679	17	US-10-027-632-102522	Sequence 102522,	621	200.2	22.1	125534	13	US-10-087-192-1678	Sequence 1678, Ap
549	200.8	22.1	679	17	US-10-027-632-102523	Sequence 102523,	622	200.2	22.1	143973	12	US-10-087-192-442	Sequence 442, Ap
550	200.8	22.1	679	17	US-10-027-632-102524	Sequence 102524,	623	200.2	22.1	150275	13	US-10-981-277-55	Sequence 55, Appl
551	200.8	22.1	696	13	US-10-027-632-212712	Sequence 212712,	624	200.2	22.1	174566	14	US-10-020-141-1	Sequence 1, Appl
552	200.8	22.1	696	17	US-10-027-632-212712	Sequence 212712,	625	200.2	22.1	174566	13	US-10-235-192A-37	Sequence 37, Appl
553	200.8	22.1	4421	14	US-10-216-372-6	Sequence 6, Appl1	626	200.2	22.1	256157	18	US-10-087-192-1204	Sequence 1204, Ap
554	200.8	22.1	17263	19	US-10-741-601-5722	Sequence 5722, Ap	627	200.2	22.1	256157	13	US-10-322-281-776	Sequence 776, Ap
555	200.8	22.1	17263	21	US-10-741-600-17846	Sequence 17846, A	628	200	22.1	626	13	US-10-027-632-133310	Sequence 133310,
556	200.8	22.1	22645	10	US-09-764-891-7673	Sequence 7673, Ap	629	200	22.1	626	17	US-10-027-632-133310	Sequence 133310,
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558	200.8	22.1	66916	19	US-10-741-601-5708	Sequence 5708, Ap	631	200	22.1	1994	13	US-10-027-632-262627	Sequence 262627,
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560	200.8	22.1	96593	18	US-10-052-482-106	Sequence 106, App	633	200	22.1	1994	13	US-10-027-632-262629	Sequence 262629,
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562	200.8	22.1	107820	19	US-10-764-328-1	Sequence 1, Appl1	635	200	22.1	1994	17	US-10-027-632-262628	Sequence 262628,
563	200.8	22.1	15053	22	US-10-981-277-36	Sequence 56, Appl	636	200	22.1	1994	17	US-10-027-632-262629	Sequence 262629,
564	200.8	22.1	172984	21	US-10-484-577-661	Sequence 661, App	637	200	22.1	2340	13	US-10-027-632-103336	Sequence 103336,
565	200.8	22.1	213040	13	US-10-087-192-856	Sequence 856, App	638	200	22.1	2340	17	US-10-027-632-103336	Sequence 103336,
566	200.8	22.1	319608	17	US-10-147-603-1	GENERAL INFORMAT	639	200	22.1	8895	9	US-09-764-855-332	Sequence 332, App
567	200.6	22.1	5668	17	US-10-074-024-751	Sequence 751, App	640	200	22.1	8895	14	US-10-072-349-332	Sequence 332, App
568	200.6	22.1	8894	9	US-09-764-847-1606	Sequence 1606, Ap	641	200	22.1	8895	17	US-10-074-024-668	Sequence 668, App
569	200.6	22.1	8894	14	US-10-092-154-1606	Sequence 1606, Ap	642	200	22.1	36110	19	US-10-741-601-5675	Sequence 5675, Ap
570	200.6	22.1	26393	15	US-10-017-161-1653	Sequence 1653, Ap	643	200	22.1	36110	20	US-10-719-993-6850	Sequence 6850, Ap
571	200.6	22.1	48680	13	US-10-087-192-2044	Sequence 2044, Ap	644	200	22.1	46649	22	US-09-805-456-3	Sequence 3, Appl1
572	200.6	22.1	49736	20	US-10-719-993-7050	Sequence 7050, Ap	645	200	22.1	46649	22	US-10-679-362-3	Sequence 3, Appl1
573	200.6	22.1	55827	9	US-09-813-133A-3	Sequence 3, Appl1	646	200	22.1	47196	21	US-10-741-600-17636	Sequence 17636, A
574	200.6	22.1	55827	14	US-10-212-877-3	Sequence 3, Appl1	647	200	22.1	50000	17	US-10-364-505-7	Sequence 7, Appl1
575	200.6	22.1	55827	21	US-10-954-110-3	Sequence 3, Appl1	648	200	22.1	50000	19	US-10-681-199-7	Sequence 7, Appl1
576	200.6	22.1	96595	17	US-10-034-650-34	Sequence 34, Appl	649	200	22.1	60330	13	US-10-087-192-1732	Sequence 1732, Ap
577	200.6	22.1	106344	10	US-09-910-185-10	Sequence 10, Appl	650	200	22.1	77992	16	US-10-225-810-11	Sequence 11, Appl
578	200.6	22.1	172569	13	US-10-087-192-1366	Sequence 1366, Ap	651	200	22.1	109906	18	US-10-235-192A-31	Sequence 31, Appl
579	200.6	22.1	172570	19	US-10-450-828-114	Sequence 114, App	652	200	22.1	161334	13	US-10-087-192-27130	Sequence 730, App
580	200.6	22.1	173308	22	US-10-756-149-629	Sequence 629, App	653	200	22.1	208700	18	US-10-388-838-4	Sequence 4, Appl1
581	200.6	22.1	246144	13	US-10-085-117-226	Sequence 226, App	654	200	22.1	304905	19	US-10-271-416-1	Sequence 1, Appl1
582	200.6	22.1	260027	17	US-10-087-192-298	Sequence 298, App	655	200	22.1	401433	22	US-10-737-082-19	Sequence 79, Appl
583	200.4	22.1	13278	18	US-10-712-363-5	Sequence 5, Appl1	656	200	22.1	401433	21	US-10-765-570-79	Sequence 79, Appl1
584	200.4	22.1	13677	18	US-10-712-363-6	Sequence 6, Appl1	657	200	22.1	653338	22	US-10-461-862-4	Sequence 4, Appl1
585	200.4	22.1	14317	20	US-10-808-522-3	Sequence 3, Appl1	658	199.8	22.0	465	19	US-10-674-124A-23132	Sequence 23132, A
586	200.4	22.1	21936	10	US-09-764-891-8807	Sequence 8807, Ap	659	199.8	22.0	560	13	US-10-027-632-276693	Sequence 276693,
587	200.4	22.1	21936	10	US-09-764-891-9446	Sequence 9446, Ap	660	199.8	22.0	560	17	US-10-027-632-276893	Sequence 276893,
588	200.4	22.1	21936	17	US-10-091-414-314	Sequence 314, App	661	199.8	22.0	614	13	US-10-027-632-287641	Sequence 287641,
589	200.4	22.1	21936	17	US-09-810-673A-3	Sequence 3, Appl1	662	199.8	22.0	614	17	US-10-027-632-287641	Sequence 287641,
590	200.4	22.1	26657	16	US-10-395-242-3	Sequence 24, Appl	663	199.8	22.0	738	13	US-10-027-632-27193	Sequence 27193, A
591	200.4	22.1	30753	22	US-10-737-082-24	Sequence 24, Appl	664	199.8	22.0	738	13	US-10-027-632-27193	Sequence 27193, A
592	200.4	22.1	30753	22	US-10-765-790-24	Sequence 24, Appl	665	199.8	22.0	738	17	US-10-027-632-27193	Sequence 27193, A
593	200.4	22.1	102730	21	US-10-367-094-153	Sequence 163, App	666	199.8	22.0	738	17	US-10-027-632-27194	Sequence 27194, A
594	200.4	22.1	109730	21	US-10-741-600-17809	Sequence 17809, A	667	199.8	22.0	2131	13	US-10-027-632-28353	Sequence 28353, A
595	200.4	22.1	142201	20	US-10-719-993-6869	Sequence 6869, Ap	668	199.8	22.0	2131	13	US-10-027-632-103101	Sequence 103101,
596	200.4	22.1	161051	20	US-10-417-375-170	Sequence 170, App	669	199.8	22.0	2131	13	US-10-027-632-103102	Sequence 103102,
597	200.4	22.1	175077	13	US-10-087-192-1168	Sequence 1168, Ap	670	199.8	22.0	2131	17	US-10-027-632-28353	Sequence 28353, A
598	200.4	22.1	183046	22	US-10-981-277-31	Sequence 31, Appl	671	199.8	22.0	2131	17	US-10-027-632-103101	Sequence 103101,
599	200.4	22.1	227968	20	US-10-723-860-1357	Sequence 1357, Ap	672	199.8	22.0	2131	17	US-10-027-632-103102	Sequence 103102,
600	200.2	22.1	283	22	US-10-984-180-1	Sequence 1, Appl1	673	199.8	22.0	2306	9	US-09-764-877-3604	Sequence 3604, Ap
601	200.2	22.1	601	19	US-10-834-850-18	Sequence 18, Appl	674	199.8	22.0	2306	17	US-10-242-515-5604	Sequence 5604, Ap
602	200.2	22.1	650	13	US-10-027-632-197409	Sequence 197409,	675	199.8	22.0	2311	9	US-09-764-877-3605	Sequence 3605, Ap
603	200.2	22.1	650	13	US-10-027-632-197410	Sequence 197410,	676	199.8	22.0	2311	17	US-10-242-515-5605	Sequence 5605, Ap
604	200.2	22.1	650	17	US-10-027-632-197409	Sequence 197409,	677	199.8	22.0	2312	9	US-09-764-877-3606	Sequence 3606, Ap
605	200.2	22.1	650	17	US-10-027-632-197410	Sequence 197410,	678	199.8	22.0	2312	17	US-10-242-515-5606	Sequence 5606, Ap
606	200.2	22.1	701	13	US-10-027-632-13809	Sequence 13809, A	679	199.8	22.0	3364	20	US-10-723-860-7092	Sequence 7092, Ap
607	200.2	22.1	701	13	US-10-027-632-13810	Sequence 13810, A	680	199.8	22.0	10024	15	US-10-017-161-1671	Sequence 1671, Ap
608	200.2	22.1	701	17	US-10-027-632-13809	Sequence 13809, A	681	199.8	22.0	10102	17	US-10-292-798-1331	Sequence 1331, Ap
609	200.2	22.1	701	17	US-10-027-632-13810	Sequence 13810, A	682	199.8	22.0	18449	9	US-09-764-866-1457	Sequence 1457, Ap
610	200.2	22.1	1032	13	US-10-027-632-116774	Sequence 116774,	683	199.8	22.0	25668	13	US-10-087-192-1444	Sequence 1444, Ap
611	200.2	22.1	1032	17	US-10-027-632-116774	Sequence 116774,	684	199.8	22.0	27246	19	US-10-741-601-5676	Sequence 5676, Ap
612	200.2	22.1	31652	21	US-10-087-192-406	Sequence 406, App	685	199.8	22.0	27246	20	US-10-719-993-6851	Sequence 6851, Ap
613	200.2	22.1	35770	23	US-10-741-600-17693	Sequence 17693, A	686	199.8	22.0	28693	21	US-10-741-600-17671	Sequence 17671, A
614	200.2	22.1	59748	19	US-10-323-281-296	Sequence 296, App	687	199.8	22.0	44851	18	US-10-719-993-6981	Sequence 6981, Ap
615	200.2	22.1	106746	20	US-10-856-888-12	Sequence 12, Appl	688	199.8	22.0	94720	20	US-10-052-482-160	Sequence 160, App
616	200.2	22.1	106746	20	US-10-856-888-12	Sequence 12, Appl	689	199.8	22.0	1229623	13	US-10-087-192-268	Sequence 268, App
617	200.2	22.1	113604	14	US-10-227-195A-1	Sequence 1, Appl1	690	199.8	22.0	131673	22	US-10-723-860-4422	Sequence 4422, Ap
618	200.2	22.1	113604	14	US-10-227-195A-2	Sequence 2, Appl1	691	199.8	22.0	131673	22	US-10-756-149-9416	Sequence 4416, Ap
619	200.2	22.1	113604	18	US-10-227-152B-1	Sequence 1, Appl1	692	199.8	22.0	155937	20	US-10-723-860-2208	Sequence 2208, Ap
620	200.2	22.1	113604	18	US-10-227-152B-2	Sequence 2, Appl1	693	199.8	22.0	160552	19	US-10-697-828-11	Sequence 11, Appl

694	199.8	22.0	170489	19	US-10-322-281-380	Sequence 380, App	676	199	21.9	32816	9	US-09-729-094-3	Sequence 3, Appl1
695	199.8	22.0	174448	13	US-10-087-192-148	Sequence 148, App	678	199	21.9	32816	16	US-10-435-631-3	Sequence 3, Appl1
696	199.6	22.0	712	17	US-10-027-632-151294	Sequence 151294, A	679	199	21.9	32816	16	US-10-435-631-3	Sequence 3, Appl1
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700	199.6	22.0	2261	17	US-10-094-745-47	Sequence 47, Appl	773	199	21.9	50927	13	US-10-367-094-56	Sequence 56, Appl
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702	199.6	22.0	3178	13	US-10-027-632-113304	Sequence 113304, A	774	199	21.9	126266	13	US-10-087-192-1132	Sequence 1132, Ap
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709	199.6	22.0	4037	21	US-09-976-674-40	Sequence 40, Appl	778	199	21.9	148567	14	US-10-254-869-3	Sequence 3, Appl1
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711	199.6	22.0	4076	21	US-10-982-512-40	Sequence 32, Appl	779	199	21.9	148567	14	US-10-254-869-3	Sequence 3, Appl1
712	199.6	22.0	4076	21	US-10-982-512-32	Sequence 32, Appl	779	199	21.9	148567	14	US-10-254-869-3	Sequence 3, Appl1
713	199.6	22.0	4100	21	US-09-976-674-38	Sequence 38, Appl	780	199	21.9	148567	14	US-10-254-869-3	Sequence 3, Appl1
714	199.6	22.0	4100	21	US-09-976-674-38	Sequence 38, Appl	780	199	21.9	148567	14	US-10-254-869-3	Sequence 3, Appl1
715	199.6	22.0	4159	21	US-09-976-674-30	Sequence 30, Appl	781	199	21.9	148567	21	US-10-965-635-3	Sequence 3, Appl1
716	199.6	22.0	4159	21	US-09-976-674-30	Sequence 30, Appl	781	199	21.9	148567	21	US-10-965-635-3	Sequence 3, Appl1
717	199.6	22.0	4180	9	US-09-976-674-36	Sequence 36, Appl	782	199	21.9	189086	13	US-10-484-577-69	Sequence 69, App
718	199.6	22.0	4180	9	US-09-976-674-36	Sequence 36, Appl	782	199	21.9	189086	13	US-10-484-577-69	Sequence 69, App
719	199.6	22.0	4219	9	US-09-976-674-28	Sequence 28, Appl	783	199	21.9	196686	13	US-10-087-192-484	Sequence 484, App
720	199.6	22.0	4219	9	US-09-976-674-28	Sequence 28, Appl	783	199	21.9	196686	13	US-10-087-192-484	Sequence 484, App
721	199.6	22.0	4263	21	US-10-982-512-28	Sequence 28, Appl	784	199	21.9	653122	13	US-10-027-632-255820	Sequence 255820, A
722	199.6	22.0	4263	21	US-10-982-512-28	Sequence 28, Appl	784	199	21.9	653122	13	US-10-027-632-255820	Sequence 255820, A
723	199.6	22.0	4302	21	US-09-976-674-24	Sequence 24, Appl	785	199.8	21.9	362	13	US-10-027-632-31274	Sequence 31274, A
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726	199.6	22.0	52745	19	US-10-741-601-5766	Sequence 5766, Ap	787	199.8	21.9	972	13	US-10-027-632-31274	Sequence 31274, A
727	199.6	22.0	116704	13	US-10-087-192-1456	Sequence 1456, Ap	788	199.8	21.9	2591	19	US-10-735-889-83	Sequence 83, Appl
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729	199.6	22.0	112976	19	US-10-367-094-99	Sequence 99, Appl	789	199.8	21.9	7152	20	US-09-829-545-29	Sequence 29, Appl
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731	199.6	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	790	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
732	199.6	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	790	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
733	199.6	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	791	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
734	199.6	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	791	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
735	199.6	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	792	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
736	199.6	22.0	1664	17	US-10-744-877-2841	Sequence 2841, Ap	792	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
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738	199.6	22.0	1756	17	US-10-108-2608-2159	Sequence 2159, Ap	793	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
739	199.6	22.0	6096	14	US-10-012-6008-1132	Sequence 1132, App	793	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
740	199.6	22.0	16815	13	US-10-017-161-1579	Sequence 1579, Ap	794	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
741	199.6	22.0	33317	13	US-10-087-192-1714	Sequence 1714, Ap	795	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
742	199.6	22.0	41694	20	US-10-719-993-6806	Sequence 6806, Ap	795	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
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745	199.6	22.0	49984	19	US-09-739-457-5	Sequence 5, Appl1	796	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
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756	199.6	22.0	61103	13	US-10-087-192-58	Sequence 58, Appl	799	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
757	199.6	22.0	61103	13	US-10-087-192-58	Sequence 58, Appl	799	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
758	199.6	22.0	66973	13	US-10-174-020-11	Sequence 11, Appl	800	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
759	199.6	22.0	66973	13	US-10-174-020-11	Sequence 11, Appl	800	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
760	199.6	22.0	95001	17	US-09-997-722-88	Sequence 88, Appl	801	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
761	199.6	22.0	95001	17	US-09-997-722-88	Sequence 88, Appl	801	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
762	199.6	22.0	95927	11	US-10-027-632-294236	Sequence 294236, A	802	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
763	199.6	22.0	95927	11	US-10-027-632-294236	Sequence 294236, A	802	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
764	199.6	22.0	597	17	US-10-027-632-294236	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
765	199.6	22.0	597	17	US-10-027-632-294236	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
766	199.6	22.0	604	17	US-10-027-632-152	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
767	199.6	22.0	604	17	US-10-027-632-152	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
768	199.6	22.0	604	17	US-10-027-632-152	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
769	199.6	22.0	604	17	US-10-027-632-152	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
770	199.6	22.0	604	17	US-10-027-632-152	Sequence 152, App	803	199.8	21.9	21470	9	US-10-668-800-29	Sequence 800, App
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841	198.6	21.9	86080	19	US-10-450-826-71	Sequence 71, Appl	c 914	198.2	21.9	21364	21	US-10-741-600-17782	Sequence 1782, A
842	198.6	21.9	86080	20	US-10-723-860-1697	Sequence 1697, Ap	c 915	198.2	21.9	29328	19	US-10-367-094-189	Sequence 189, App
843	198.6	21.9	86080	22	US-10-756-149-1653	Sequence 1653, Ap	c 916	198.2	21.9	32194	10	US-09-764-891-1028	Sequence 7028, Ap
844	198.6	21.9	106378	13	US-10-087-192-1624	Sequence 1624, Ap	c 917	198.2	21.9	37940	17	US-10-348-073A-12	Sequence 12, Appl
c 845	198.6	21.9	106707	19	US-10-694-685-8	Sequence 8, Appl1	c 918	198.2	21.9	38000	17	US-10-175-627-11	Sequence 11, Appl1
c 846	198.6	21.9	118466	21	US-10-461-863-86	Sequence 86, Appl	c 919	198.2	21.9	40987	21	US-10-741-601-5703	Sequence 5703, Ap
c 847	198.6	21.9	145806	20	US-10-719-993-6943	Sequence 6943, Ap	c 920	198.2	21.9	40987	21	US-10-741-600-18008	Sequence 18008, A
848	198.6	21.9	145831	9	US-09-969-108-79	Sequence 79, Appl	c 921	198.2	21.9	41866	13	US-10-087-192-1804	Sequence 1804, Ap
849	198.6	21.9	145831	10	US-09-954-456-2116	Sequence 2116, Ap	c 922	198.2	21.9	50000	17	US-10-364-505-7	Sequence 7, Appl1
850	198.6	21.9	145831	9	US-09-873-367C-646	Sequence 646, App	c 923	198.2	21.9	50000	19	US-10-681-199-7	Sequence 7, Appl1
851	198.6	21.9	145831	11	US-09-968-007A-455	Sequence 455, App	c 924	198.2	21.9	55346	20	US-10-719-993-7052	Sequence 7052, Ap
852	198.6	21.9	145831	18	US-10-240-427-363	Sequence 363, App	c 925	198.2	21.9	62124	20	US-10-417-375-82	Sequence 82, Appl
853	198.6	21.9	145831	21	US-10-843-644A-646	Sequence 646, App	c 927	198.2	21.9	115756	22	US-10-756-149-1838	Sequence 1838, Ap
854	198.6	21.9	145831	21	US-10-843-644A-5143	Sequence 5143, Ap	c 927	198.2	21.9	123326	20	US-09-910-185-11	Sequence 11, Appl
855	198.6	21.9	145831	21	US-10-843-644A-5925	Sequence 6925, Ap	c 928	198.2	21.9	202814	20	US-10-719-993-6812	Sequence 6812, Ap
856	198.6	21.9	145831	22	US-10-843-644A-7550	Sequence 7550, Ap	c 929	198.2	21.9	246640	19	US-10-332-666-58	Sequence 58, Appl
857	198.6	21.9	145831	22	US-10-756-149-921	Sequence 921, App	c 930	198.2	21.9	317876	21	US-10-741-601-5629	Sequence 5629, Ap
858	198.6	21.9	154875	22	US-10-737-082-107	Sequence 107, App	c 931	198.2	21.9	317876	21	US-10-741-600-17607	Sequence 17607, A
859	198.6	21.9	154875	22	US-10-765-799-107	Sequence 107, App	c 932	198.2	21.9	368004	9	US-09-949-654-3	Sequence 3, Appl1
860	198.6	21.9	36803	20	US-10-719-993-6805	Sequence 6805, App	c 933	198.2	21.9	383432	22	US-10-737-082-34	Sequence 34, Appl
c 861	198.6	21.9	410846	21	US-10-481-613-1	Sequence 1, Appl1	c 934	198.2	21.9	383432	22	US-10-765-799-34	Sequence 1463, Ap
c 862	198.4	21.9	291	16	US-10-229-058B-15	Sequence 15, Appl	c 935	198.2	21.9	418550	20	US-10-292-798-1463	Sequence 6817, Ap
c 863	198.4	21.9	638	13	US-10-027-632-234365	Sequence 234365,	c 936	198.2	21.9	717651	20	US-10-719-993-6817	Sequence 33, Appl
c 864	198.4	21.9	638	13	US-10-027-632-234366	Sequence 234366,	c 937	198.2	21.8	493	22	US-10-933-118-33	Sequence 187116,
c 865	198.4	21.9	638	13	US-10-027-632-234367	Sequence 234367,	c 938	198.2	21.8	572	13	US-10-027-632-187116	Sequence 187116,
c 866	198.4	21.9	638	13	US-10-027-632-234368	Sequence 234368,	c 939	198.2	21.8	572	17	US-10-027-632-187116	Sequence 142951,
c 867	198.4	21.9	638	13	US-10-027-632-234369	Sequence 234369,	c 940	198.2	21.8	705	13	US-10-027-632-142951,	Sequence 142951,
c 868	198.4	21.9	638	17	US-10-027-632-234365	Sequence 234365,	c 941	198.2	21.8	705	17	US-10-027-632-142951,	Sequence 162285,
c 869	198.4	21.9	638	17	US-10-027-632-234366	Sequence 234366,	c 942	198.2	21.8	825	13	US-10-027-632-162285,	Sequence 162285,
c 870	198.4	21.9	638	17	US-10-027-632-234367	Sequence 234367,	c 943	198.2	21.8	825	17	US-10-027-632-162285,	Sequence 162285,
c 871	198.4	21.9	638	17	US-10-027-632-234368	Sequence 234368,	c 944	198.2	21.8	1204	13	US-10-027-632-118994,	Sequence 118994,
c 872	198.4	21.9	638	17	US-10-027-632-234369	Sequence 234369,	c 945	198.2	21.8	1204	17	US-10-027-632-118994,	Sequence 7028, Ap
873	198.4	21.9	826	13	US-10-027-632-8234	Sequence 8234, Ap	c 946	198.2	21.8	1211	20	US-10-723-860-7028	Sequence 7028, Ap
874	198.4	21.9	826	17	US-10-027-632-8234	Sequence 8234, Ap	c 947	198.2	21.8	2460	17	US-10-108-260A-595	Sequence 595, App
875	198.4	21.9	1295	13	US-10-027-632-133215	Sequence 133215,	c 948	198.2	21.8	3448	13	US-10-027-632-115054	Sequence 115054,
876	198.4	21.9	1295	13	US-10-027-632-133216	Sequence 133216,	c 949	198.2	21.8	3448	17	US-10-027-632-115054	Sequence 115054,
877	198.4	21.9	1295	13	US-10-027-632-133217	Sequence 133217,	c 950	198.2	21.8	9432	14	US-09-942-310-1	Sequence 1, Appl1
878	198.4	21.9	1295	17	US-10-027-632-133215	Sequence 133215,	c 951	198.2	21.8	9432	14	US-10-209-737-1	Sequence 1, Appl1
879	198.4	21.9	1295	17	US-10-027-632-133216	Sequence 133216,	c 952	198.2	21.8	9432	18	US-10-712-363-1	Sequence 1, Appl1
880	198.4	21.9	1295	17	US-10-027-632-133217	Sequence 133217,	c 953	198.2	21.8	9433	18	US-10-209-737-2	Sequence 2, Appl1
881	198.4	21.9	1672	9	US-09-764-847-1183	Sequence 1183, Ap	c 954	198.2	21.8	9609	21	US-10-635-780-4	Sequence 4, Appl1
882	198.4	21.9	1672	14	US-10-092-154-1183	Sequence 1183, Ap	c 955	198.2	21.8	11557	9	US-09-764-856-103	Sequence 103, App
c 883	198.4	21.9	2549	17	US-10-108-260A-1413	Sequence 1413, Ap	c 956	198.2	21.8	11557	9	US-09-764-856-103	Sequence 104, App
c 884	198.4	21.9	3310	22	US-10-756-149-592	Sequence 592, App	c 957	198.2	21.8	11557	10	US-09-764-881-8063	Sequence 9063, Ap
885	198.4	21.9	22186	17	US-10-085-117-178	Sequence 178, App	c 958	198.2	21.8	11557	11	US-09-764-881-8064	Sequence 1064, Ap
886	198.4	21.9	23013	21	US-10-741-600-17898	Sequence 17898, A	c 959	198.2	21.8	11557	11	US-09-764-881-8064	Sequence 1064, Ap
887	198.4	21.9	25322	21	US-10-741-600-17737	Sequence 17737, A	c 960	198.2	21.8	11557	14	US-10-102-627-103	Sequence 103, App
888	198.4	21.9	86081	19	US-10-741-601-5640	Sequence 5640, Ap	c 961	198.2	21.8	11557	14	US-10-102-627-103	Sequence 104, App
889	198.4	21.9	86081	21	US-10-741-600-17633	Sequence 17633, A	c 962	198.2	21.8	11557	14	US-10-102-627-104	Sequence 104, App
c 890	198.4	21.9	87687	13	US-10-087-192-178	Sequence 178, App	c 963	198.2	21.8	19772	9	US-09-764-864-1698	Sequence 1698, Ap
891	198.4	21.9	87689	19	US-10-717-597-194	Sequence 194, App	c 964	198.2	21.8	32134	10	US-09-764-881-5303	Sequence 6303, Ap
892	198.4	21.9	95835	13	US-10-087-192-1792	Sequence 1792, Ap	c 965	198.2	21.8	32134	15	US-10-205-428-008	Sequence 608, App
893	198.4	21.9	128034	17	US-10-282-174-187	Sequence 187, App	c 966	198.2	21.8	32134	15	US-09-764-881-5304	Sequence 6304, App
894	198.4	21.9	128034	21	US-10-600-009-187	Sequence 187, App	c 967	198.2	21.8	32191	15	US-10-205-428-009	Sequence 609, App
895	198.4	21.9	143899	21	US-09-972-546-15	Sequence 15, Appl	c 968	198.2	21.8	39898	21	US-10-741-600-17632	Sequence 17632, A
896	198.4	21.9	143899	21	US-10-735-266-15	Sequence 15, Appl	c 969	198.2	21.8	40000	21	US-10-741-600-18015	Sequence 18015, A
897	198.4	21.9	174424	9	US-09-967-768A-314	Sequence 314, App	c 970	198.2	21.8	40045	9	US-09-818-656A-3	Sequence 3, Appl1
898	198.4	21.9	174424	10	US-09-960-706-969	Sequence 969, App	c 971	198.2	21.8	40645	9	US-10-216-441-3	Sequence 3, Appl1
899	198.4	21.9	174424	21	US-10-843-641A-6459	Sequence 6459, Ap	c 972	198.2	21.8	40645	22	US-10-961-230-3	Sequence 3, Appl1
900	198.4	21.9	181343	21	US-10-723-860A-2392	Sequence 2392, Ap	c 973	198.2	21.8	55114	22	US-10-087-192-1606	Sequence 1606, Ap
901	198.4	21.9	181343	22	US-10-756-149-2215	Sequence 2215, Ap	c 974	198.2	21.8	59817	18	US-10-052-482-190	Sequence 190, App
902	198.4	21.9	203654	9	US-09-820-905-3	Sequence 3, Appl1	c 975	198.2	21.8	70000	20	US-10-476-991-3	Sequence 3, Appl1
903	198.4	21.9	203654	22	US-10-473-338A-3	Sequence 3, Appl1	c 976	198.2	21.8	73771	13	US-10-087-192-1636	Sequence 1636, Ap
904	198.2	21.9	1326	13	US-10-027-632-132225	Sequence 132225,	c 977	198.2	21.8	110665	22	US-10-723-860-1802	Sequence 1802, Ap
905	198.2	21.9	1326	13	US-10-027-632-132226	Sequence 132226,	c 978	198.2	21.8	110665	22	US-10-756-149-1888	Sequence 1888, Ap
906	198.2	21.9	1326	17	US-10-027-632-132225	Sequence 132225,	c 979	198.2	21.8	114771	20	US-10-723-860-458	Sequence 458, App
907	198.2	21.9	1326	17	US-10-027-632-132226	Sequence 132226,	c 980	198.2	21.8	132762	17	US-09-954-556-17	Sequence 17, Appl
908	198.2	21.9	2062	17	US-10-108-260A-1541	Sequence 1541, Ap	c 981	198.2	21.8	146671	17	US-10-226-031B-53	Sequence 53, Appl
909	198.2	21.9	2541	9	US-09-823-245A-569	Sequence 569, App	c 982	198.2	21.8	159204	22	US-10-756-149-1804	Sequence 3804, Ap
910	198.2	21.9	4824	9	US-09-960-253-160	Sequence 160, App	c 983	198.2	21.8	410846	21	US-10-481-613-1	Sequence 1, Appl1
911	198.2	21.9	4824	15	US-10-171-581-82	Sequence 82, Appl	c 984	198.2	21.8	606398	20	US-10-719-993-6782	Sequence 6782, Ap
912	198.2	21.9	4885	22	US-10-220-335-81	Sequence 81, Appl	c 985	197.8	21.8	648	13	US-10-027-632-107015	Sequence 107015,

c 986	197.8	21.8	648	17	US-10-027-632-107015	Sequence 107015,	1059	197.4	21.8	1449	21	US-10-087-553A-909	Sequence 909, App
c 987	197.8	21.8	1167	22	US-10-499-353A-2	Sequence 2,	1060	197.4	21.8	1449	21	US-10-956-157-2117	Sequence 2117, Ap
c 988	197.8	21.8	1167	22	US-09-735-103-9	Sequence 9, Appl1	1061	197.4	21.8	1453	21	US-10-153-666-439	Sequence 439, App
c 989	197.8	21.8	3129	13	US-10-045-428A-9	Sequence 9, Appl1	c1062	197.4	21.8	1463	19	US-10-741-601-5776	Sequence 5776, Ap
c 990	197.8	21.8	3705	10	US-09-822-846-279	Sequence 279, App	1063	197.4	21.8	23469	19	US-10-741-601-5659	Sequence 5659, Ap
c 991	197.8	21.8	6610	13	US-10-098-841-139	Sequence 139, App	c1064	197.4	21.8	33175	19	US-10-741-601-5651	Sequence 5651, Ap
c 992	197.8	21.8	21913	10	US-09-764-891-6085	Sequence 6085, Ap	c1065	197.4	21.8	45656	20	US-10-719-993-6910	Sequence 6910, Ap
c 993	197.8	21.8	21913	10	US-09-764-891-6067	Sequence 6067, Ap	c1066	197.4	21.8	45656	20	US-10-741-600-17829	Sequence 17829, A
c 994	197.8	21.8	21913	10	US-09-764-891-6067	Sequence 6067, Ap	c1067	197.4	21.8	52710	19	US-10-322-281-572	Sequence 572, App
c 995	197.8	21.8	25001	17	US-10-187-659A-11	Sequence 11, Appl1	1068	197.4	21.8	61765	13	US-10-322-281-624	Sequence 624, App
996	197.8	21.8	28616	17	US-10-455-552-1	Sequence 11, Appl1	1069	197.4	21.8	68255	19	US-10-087-192-772	Sequence 772, App
997	197.8	21.8	32121	17	US-10-074-024-446	Sequence 446, App	c1070	197.4	21.8	117231	22	US-10-893-315-129	Sequence 129, App
c 998	197.8	21.8	32855	13	US-10-087-192-964	Sequence 964, App	c1071	197.4	21.8	174424	9	US-09-967-768A-314	Sequence 314, App
c 999	197.8	21.8	53522	10	US-09-904-968A-1	Sequence 1, Appl1	c1072	197.4	21.8	174424	21	US-10-843-661A-6459	Sequence 6459, App
c1000	197.8	21.8	70242	13	US-10-087-192-1294	Sequence 1294, Ap	c1073	197.4	21.8	174434	20	US-10-723-860A-2392	Sequence 2392, Ap
c1001	197.8	21.8	96256	19	US-10-087-192-352	Sequence 352, App	c1074	197.4	21.8	181343	20	US-10-723-860A-2392	Sequence 2392, Ap
c1002	197.8	21.8	98716	21	US-10-741-600-17754	Sequence 17754, A	c1075	197.4	21.8	181343	22	US-10-756-149-2215	Sequence 2215, Ap
c1003	197.8	21.8	103660	16	US-10-741-600-17645	Sequence 17645, A	c1076	197.4	21.8	187844	20	US-10-719-993-6683	Sequence 6683, Ap
c1004	197.8	21.8	113000	16	US-10-576-566-16	Sequence 16, Appl1	1077	197.4	21.8	214000	21	US-10-829-674-1	Sequence 1, Appl1
c1005	197.8	21.8	128034	21	US-10-600-009-186	Sequence 186, App	1078	197.4	21.8	214000	21	US-10-830-477-1	Sequence 1, Appl1
c1006	197.8	21.8	128034	21	US-10-600-009-186	Sequence 186, App	1079	197.4	21.8	447894	21	US-10-723-670-1	Sequence 1, Appl1
c1007	197.8	21.8	128668	13	US-10-087-192-340	Sequence 340, App	c1080	197.4	21.7	465237	9	US-09-933-267A-1	Sequence 1, Appl1
c1008	197.8	21.8	134292	18	US-10-240-425-1102	Sequence 1102, Ap	c1081	197.2	21.7	402	19	US-10-674-128A-386	Sequence 386, App
c1009	197.8	21.8	134292	21	US-10-278-698-335	Sequence 335, App	c1082	197.2	21.7	600	21	US-10-956-157-7721	Sequence 7721, Ap
c1010	197.8	21.8	134292	21	US-10-278-698-335	Sequence 335, App	c1083	197.2	21.7	648	13	US-10-027-632-112653	Sequence 112653, App
c1011	197.8	21.8	162450	15	US-10-071-179-1	Sequence 1, Appl1	c1084	197.2	21.7	648	13	US-10-027-632-112653	Sequence 112653, App
c1012	197.8	21.8	162450	16	US-10-126-704-1	Sequence 1, Appl1	c1085	197.2	21.7	648	17	US-10-027-632-112654	Sequence 112654, App
c1013	197.8	21.8	202100	21	US-10-282-174-484	Sequence 484, App	c1086	197.2	21.7	648	17	US-10-027-632-112654	Sequence 112654, App
c1014	197.8	21.8	202100	21	US-10-600-009-484	Sequence 484, App	1087	197.2	21.7	751	17	US-09-953-318-20	Sequence 20, Appl1
c1015	197.8	21.8	253439	15	US-10-719-993-6799	Sequence 6799, Ap	1088	197.2	21.7	751	17	US-10-446-373-20	Sequence 20, Appl1
c1016	197.8	21.8	300000	15	US-10-262-552-33	Sequence 33, Appl1	1089	197.2	21.7	854	13	US-10-027-632-162774	Sequence 162774, App
c1017	197.8	21.8	300000	19	US-10-703-210-33	Sequence 33, Appl1	1090	197.2	21.7	854	17	US-10-027-632-162774	Sequence 162774, App
c1018	197.8	21.8	335791	11	US-09-768-185A-1	Sequence 1, Appl1	1091	197.2	21.7	2052	21	US-10-956-157-2486	Sequence 2486, Ap
c1019	197.6	21.8	601	9	US-09-818-656A-60	Sequence 60, Appl1	1092	197.2	21.7	2052	21	US-10-956-157-2486	Sequence 2486, Ap
c1020	197.6	21.8	601	9	US-09-818-656A-62	Sequence 62, Appl1	c1093	197.2	21.7	33478	10	US-10-322-281-188	Sequence 188, App
c1021	197.6	21.8	2702	10	US-09-822-846-142	Sequence 142, App	c1094	197.2	21.7	33478	10	US-10-898-406-3	Sequence 3, Appl1
c1022	197.6	21.8	12586	21	US-10-741-600-17608	Sequence 17608, A	1095	197.2	21.7	35804	21	US-10-989-406-3	Sequence 3, Appl1
c1023	197.6	21.8	23626	9	US-09-764-878-261	Sequence 261, App	c1096	197.2	21.7	40433	9	US-09-880-107-3327	Sequence 3327, Ap
c1024	197.6	21.8	23626	9	US-09-764-860-940	Sequence 940, App	c1097	197.2	21.7	40433	22	US-10-756-149-1455	Sequence 1455, Ap
c1025	197.6	21.8	23626	14	US-10-079-854-261	Sequence 261, App	c1098	197.2	21.7	57759	22	US-10-783-271-108	Sequence 108, App
c1026	197.6	21.8	23626	14	US-10-074-095-940	Sequence 940, App	c1099	197.2	21.7	57759	18	US-10-052-482-34	Sequence 34, Appl1
c1027	197.6	21.8	23626	14	US-10-074-095-940	Sequence 940, App	c1100	197.2	21.7	70000	17	US-10-012-723-13	Sequence 13, Appl1
c1028	197.6	21.8	23626	14	US-10-212-872-950	Sequence 212, App	c1101	197.2	21.7	92139	6	US-09-918-686-1	Sequence 1, Appl1
c1029	197.6	21.8	23632	9	US-09-764-878-362	Sequence 262, App	c1102	197.2	21.7	92139	16	US-10-353-150-1	Sequence 1, Appl1
c1030	197.6	21.8	23632	14	US-10-079-854-262	Sequence 941, App	c1103	197.2	21.7	130320	17	US-10-408-168-1	Sequence 1, Appl1
c1031	197.6	21.8	23632	17	US-10-074-095-941	Sequence 941, App	c1104	197.2	21.7	166436	22	US-10-756-149-590	Sequence 590, App
c1032	197.6	21.8	23632	17	US-10-074-095-941	Sequence 941, App	c1105	197.2	21.7	166436	22	US-10-981-27-42	Sequence 42, App
c1033	197.6	21.8	23632	17	US-10-074-095-941	Sequence 941, App	c1106	197.2	21.7	317129	21	US-10-741-600-17765	Sequence 17765, A
c1034	197.6	21.8	23632	17	US-10-074-095-941	Sequence 941, App	c1107	197.2	21.7	317129	21	US-10-087-192-250	Sequence 250, App
c1035	197.6	21.8	23632	17	US-10-074-095-941	Sequence 941, App	c1108	197.2	21.7	567564	19	US-10-699-156-3	Sequence 3, Appl1
c1036	197.6	21.8	52987	19	US-10-322-281-1030	Sequence 1030, Ap	c1109	197.2	21.7	705	13	US-10-027-632-104432	Sequence 104432, App
c1037	197.6	21.8	52987	19	US-10-322-281-1030	Sequence 386, App	c1110	197.2	21.7	705	13	US-10-027-632-1142952	Sequence 142952, App
c1038	197.6	21.8	52987	19	US-10-322-281-1030	Sequence 386, App	c1111	197.2	21.7	705	13	US-10-027-632-123526	Sequence 123526, App
c1039	197.6	21.8	52987	19	US-10-322-281-1030	Sequence 386, App	c1112	197.2	21.7	705	13	US-10-027-632-123526	Sequence 123526, App
c1040	197.6	21.8	52987	19	US-10-322-281-1030	Sequence 386, App	c1113	197.2	21.7	705	17	US-10-027-632-123526	Sequence 123526, App
c1041	197.6	21.8	175737	22	US-10-783-192-34	Sequence 34, Appl1	c1114	197.2	21.7	1515	17	US-10-074-024-684	Sequence 684, App
c1042	197.6	21.8	198522	13	US-10-087-192-34	Sequence 244, App	c1115	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1043	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1116	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1044	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1117	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1045	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1118	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1046	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1119	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1047	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1120	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1048	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1121	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1049	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1122	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1050	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1123	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1051	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1124	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1052	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1125	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1053	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1126	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1054	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1127	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1055	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1128	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1056	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1129	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1057	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1130	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1
c1058	197.6	21.8	260209	15	US-10-265-071-23	Sequence 23, Appl1	c1131	197.2	21.7	2818	20	US-10-602-494-25	Sequence 25, Appl1

c1132	197	21.7	96588	17	US-10-085-117-76	Sequence 76, Appl
c1133	197	21.7	114931	13	US-10-087-192-862	Sequence 862, App
c1134	197	21.7	116782	13	US-10-087-192-1090	Sequence 1090, Ap
c1135	197	21.7	119501	17	US-10-174-319-15	Sequence 15, Appl
c1136	197	21.7	119596	14	US-10-270-336-3	Sequence 3, Appl1
c1137	197	21.7	128034	17	US-10-282-174-166	Sequence 186, App
c1138	197	21.7	128034	17	US-10-282-174-187	Sequence 187, App
c1139	197	21.7	128034	21	US-10-600-009-186	Sequence 186, App
c1140	197	21.7	128034	21	US-10-600-009-187	Sequence 187, App
c1141	197	21.7	128034	22	US-10-756-149-3773	Sequence 3773, Ap
c1142	197	21.7	155074	13	US-10-026-188-6	Sequence 6, Appl1
c1143	197	21.7	166181	20	US-10-723-860-1452	Sequence 1452, Ap
c1144	197	21.7	166181	20	US-10-723-860-3281	Sequence 3281, Ap
c1145	197	21.7	174448	13	US-10-087-192-148	Sequence 148, App
c1146	197	21.7	193691	20	US-10-719-993-6768	Sequence 6768, Ap
c1147	197	21.7	212231	13	US-10-087-192-1126	Sequence 1126, Ap
c1148	197	21.7	231914	21	US-10-741-600-17654	Sequence 17654, A
c1149	197	21.7	275449	13	US-10-087-192-520	Sequence 520, App
c1150	196.8	21.7	887	13	US-10-027-632-156972	Sequence 156972, Sequence 156972,
c1151	196.8	21.7	887	13	US-10-027-632-156973	Sequence 156973,
c1152	196.8	21.7	887	13	US-10-027-632-156974	Sequence 156974,
c1153	196.8	21.7	887	17	US-10-027-632-156972	Sequence 156972,
c1154	196.8	21.7	887	17	US-10-027-632-156973	Sequence 156973,
c1155	196.8	21.7	887	17	US-10-027-632-156974	Sequence 156974,
c1156	196.8	21.7	943	13	US-10-027-632-122182	Sequence 122182,
c1157	196.8	21.7	943	17	US-10-027-632-122182	Sequence 122182,
c1158	196.8	21.7	2308	17	US-10-104-047-682	Sequence 682, App
c1159	196.8	21.7	2404	17	US-10-108-260A-1180	Sequence 1180, Ap
c1160	196.8	21.7	6833	20	US-10-723-860-6965	Sequence 6965, Ap
c1161	196.8	21.7	6833	20	US-10-723-860-7739	Sequence 7739, Ap
c1162	196.8	21.7	7444	10	US-09-764-891-8806	Sequence 8806, Ap
c1163	196.8	21.7	7444	10	US-09-764-891-9448	Sequence 9448, Ap
c1164	196.8	21.7	7444	9	US-10-091-414-316	Sequence 316, App
c1165	196.8	21.7	9765	9	US-09-764-853-888	Sequence 888, App
c1166	196.8	21.7	9765	9	US-09-764-853-935	Sequence 935, App
c1167	196.8	21.7	9765	14	US-10-091-438-248	Sequence 248, App
c1168	196.8	21.7	9765	14	US-10-091-438-257	Sequence 257, App
c1169	196.8	21.7	21704	15	US-10-017-161-709	Sequence 709, App
c1170	196.8	21.7	21704	17	US-10-292-798-621	Sequence 621, App
c1171	196.8	21.7	27847	14	US-10-263-593-3	Sequence 3, Appl1
c1172	196.8	21.7	32192	9	US-09-764-877-3657	Sequence 3657, Ap
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c1175	196.8	21.7	35641	9	US-09-962-436-306	Sequence 306, App
c1176	196.8	21.7	35641	9	US-09-880-107-2225	Sequence 2225, Ap
c1177	196.8	21.7	35641	21	US-10-843-641A-2765	Sequence 2765, Ap
c1178	196.8	21.7	37925	11	US-09-984-429-701	Sequence 701, App
c1179	196.8	21.7	39105	21	US-10-741-600-17653	Sequence 17653, A
c1180	196.8	21.7	44325	11	US-09-997-722-226	Sequence 226, App
c1181	196.8	21.7	45944	19	US-10-367-094-38	Sequence 38, Appl
c1182	196.8	21.7	59463	17	US-10-085-117-184	Sequence 184, App
c1183	196.8	21.7	67253	22	US-10-737-082-88	Sequence 88, Appl
c1184	196.8	21.7	67253	22	US-10-765-790-88	Sequence 88, Appl
c1185	196.8	21.7	67858	21	US-10-741-600-17974	Sequence 17974, A
c1186	196.8	21.7	70000	20	US-10-476-991-3	Sequence 3, Appl1
c1187	196.8	21.7	80399	20	US-10-719-993-6831	Sequence 6831, Ap
c1188	196.8	21.7	106938	19	US-10-322-281-566	Sequence 566, App
c1189	196.8	21.7	116327	20	US-10-719-993-6867	Sequence 6867, Ap
c1190	196.8	21.7	145806	20	US-10-719-993-6943	Sequence 6943, Ap
c1191	196.8	21.7	158001	22	US-10-211-179-11	GENERAL INFORMATI
c1192	196.8	21.7	165097	22	US-10-737-082-77	Sequence 77, Appl
c1193	196.8	21.7	165097	22	US-10-765-790-77	Sequence 77, Appl
c1194	196.8	21.7	201239	21	US-10-278-698-246	Sequence 246, App
c1195	196.8	21.7	201239	21	US-10-278-698-760	Sequence 760, App
c1196	196.8	21.7	201239	21	US-10-719-993-6876	Sequence 6876, Ap
c1197	196.8	21.7	606398	20	US-10-719-993-6782	Sequence 6782, Ap
c1198	196.6	21.7	288	14	US-10-115-278-2	Sequence 2, Appl1
c1199	196.6	21.7	288	10	US-10-762-966-2	Sequence 2, Appl1
c1200	196.6	21.7	461	9	US-09-884-441-1	Sequence 1, Appl1
c1201	196.6	21.7	461	9	US-09-884-441-3	Sequence 3, Appl1
c1202	196.6	21.7	461	10	US-09-907-969-1	Sequence 1, Appl1
c1203	196.6	21.7	461	10	US-09-907-969-3	Sequence 3, Appl1
c1204	196.6	21.7	461	10	US-09-827-271-1	Sequence 1, Appl1

c1205	196.6	21.7	461	10	US-09-827-271-3	Sequence 3, Appl1
c1206	196.6	21.7	461	15	US-10-198-053-1	Sequence 1, Appl1
c1207	196.6	21.7	461	21	US-10-198-053-3	Sequence 3, Appl1
c1208	196.6	21.7	461	21	US-10-860-790-1	Sequence 1, Appl1
c1209	196.6	21.7	461	21	US-10-860-790-3	Sequence 3, Appl1
c1210	196.6	21.7	571	13	US-10-027-632-252752	Sequence 252752,
c1211	196.6	21.7	571	17	US-10-027-632-252752	Sequence 252752,
c1212	196.6	21.7	2255	13	US-10-027-632-110965	Sequence 110965,
c1213	196.6	21.7	2255	17	US-10-027-632-110965	Sequence 110965,

Search completed: September 15, 2005, 20:27:59
Job time : 867 secs

Run on: September 15, 2005, 13:47:33 ; Search time 617 Seconds
(without alignments)

8702.116 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 1 ggaactctgaaggtcccaagc.....gtgagactcaccatcacaca 907

Sequence: IDENTITY_NNC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : N_Geneseq_16Dec04:*

Listing first 1500 summaries

1: geneseqn19808:*

2: geneseqn19908:*

3: geneseqn20008:*

4: geneseqn20018:*

5: geneseqn20028:*

6: geneseqn20038:*

7: geneseqn20048:*

8: geneseqn20058:*

9: geneseqn20068:*

10: geneseqn20078:*

11: geneseqn20088:*

12: geneseqn20098:*

13: geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description

NO.	Score	Match	Length	DB	ID	ID	Description
RESULT 1	100.0%	Score 907;	DB 3;	Length 907;			
ID	AAZ65100	standard;	CDNA;	907 BP.			
DE	Membrane-bound protein PRO1187 encoding CDNA.						
PN	WO963088-A2.						
PD	08-DEC-1999.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 3;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 2	100.0%	Score 907;	DB 3;	Length 907;			
ID	AAC58387	standard;	CDNA;	907 BP.			
DE	Human PRO1187 nucleotide sequence SEQ ID NO:54.						
PN	WO200053755-A2.						
PD	14-SEP-2000.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 3;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 3	100.0%	Score 907;	DB 3;	Length 907;			
ID	AAAF44246	standard;	CDNA;	907 BP.			
DE	Human PRO1187 (UNQ601) nucleotide sequence SEQ ID NO:398.						
PN	WO200073454-A1.						
PD	07-DEC-2000.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 5;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 4	100.0%	Score 907;	DB 6;	Length 907;			
ID	ABK33584	standard;	CDNA;	907 BP.			
DE	CDNA encoding human PRO protein, Seq ID NO 97.						
PN	WO200208288-A2.						
PD	31-JAN-2002.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 6;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 5	100.0%	Score 907;	DB 6;	Length 907;			
ID	ACA64425	standard;	CDNA;	907 BP.			
DE	Novel human secreted and transmembrane protein PRO1187 CDNA.						
PN	US2003003531-A1.						
PD	02-JAN-2003.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 6	100.0%	Score 907;	DB 8;	Length 907;			
ID	ABX80884	standard;	CDNA;	907 BP.			
DE	Human secreted/transmembrane protein CDNA, #160.						
PN	US2003027162-A1.						
PD	06-FEB-2003.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 7	100.0%	Score 907;	DB 8;	Length 907;			
ID	ACD44393	standard;	CDNA;	907 BP.			
DE	CDNA encoding human PRO1187 polypeptide.						
PN	US2002127576-A1.						
PD	12-SEP-2002.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 8	100.0%	Score 907;	DB 8;	Length 907;			
ID	ACA65545	standard;	CDNA;	907 BP.			
DE	Novel human secreted and transmembrane protein PRO1187 CDNA.						
PN	US2003088063-A1.						
PD	08-MAY-2003.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 9	100.0%	Score 907;	DB 8;	Length 907;			
ID	ABX79564	standard;	CDNA;	907 BP.			
DE	Human secreted/transmembrane protein CDNA, #160.						
PN	US2002142961-A1.						
PD	03-OCT-2002.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 10	100.0%	Score 907;	DB 8;	Length 907;			
ID	ACA93585	standard;	CDNA;	907 BP.			
DE	Novel human secreted and transmembrane protein PRO1187 CDNA.						
PN	US2003022187-A1.						
PD	30-JAN-2003.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 11	100.0%	Score 907;	DB 8;	Length 907;			
ID	ABX81267	standard;	DNA;	907 BP.			
DE	Novel human secreted or transmembrane protein PRO1185 DNA.						
PN	US2003027985-A1.						
PD	06-FEB-2003.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 12	100.0%	Score 907;	DB 8;	Length 907;			
ID	ACA93083	standard;	CDNA;	907 BP.			
DE	Novel human secreted and transmembrane protein PRO1187 CDNA.						
PN	US2003017476-A1.						
PD	23-JAN-2003.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 13	100.0%	Score 907;	DB 8;	Length 907;			
ID	ABX17167	standard;	CDNA;	907 BP.			
DE	Human PRO polynucleotide #124.						
PN	US2002123463-A1.						
PD	05-SEP-2002.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 8;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 14	100.0%	Score 907;	DB 8;	Length 907;			
ID	ACA68022	standard;	CDNA;	907 BP.			
DE	Novel human secreted and transmembrane protein PRO1187 CDNA.						
PN	US2002177164-A1.						
PD	28-NOV-2002.						
PA	(GETH) GENENTECH INC.						
Query Match	100.0%;	Score 907;	DB 9;	Length 907;			
Best Local Similarity	100.0%;	Pred. No. 2.6e-250;					
RESULT 15	100.0%	Score 907;	DB 9;	Length 907;			
ID	ACA88471	standard;	CDNA;	907 BP.			
DE	Human secreted and transmembrane polypeptide PRO1187 CDNA.						

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PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 16
ID ACD81978 standard; cDNA; 907 BP.
DE Human cDNA encoding human PRO1187 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 17
ID ABT44274 standard; cDNA; 907 BP.
DE Human PRO1187 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 18
ID ADA37909 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 19
ID ADA21595 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1187.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 20
ID ADA10382 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1187.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 21
ID ADA17926 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 22
ID ADA28034 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 23
ID ADA9614 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 24
ID ADA3839 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 25
ID ABT44557 standard; cDNA; 907 BP.
DE Human PRO1187 cDNA.
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PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 26
ID ADA92960 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 27
ID ACD82224 standard; cDNA; 907 BP.
DE Human secreted/transmembrane polypeptide PRO 1187 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 28
ID ACH65539 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 29
ID ADA22521 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1187.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 30
ID ACD39529 standard; cDNA; 907 BP.
DE Human cDNA encoding PRO1185.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 31
ID ADA06687 standard; cDNA; 907 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #124.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 32
ID ABT43930 standard; cDNA; 907 BP.
DE Human membrane bound receptor/protein PRO1187 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 33
ID ADA39380 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 34
ID ADB83587 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 35
ID ADB80693 standard; cDNA; 907 BP.
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DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 36
ID ADB72324 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003086968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 37
ID ADB96406 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003054403-A1.
PD 20-MAR-2003.
PA Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 38
ID ADB78316 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 39
ID ADB84964 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 40
ID ADB78070 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 41
ID ADB87136 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 42
ID ADB84718 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 43
ID ADB83833 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US200306397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 44
ID ADB72988 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092887-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 45
ID ADC57878 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003027754-A1.
PD 06-FEB-2003.
PA Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 46
ID ADC55242 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003045463-A1.
PD 06-MAR-2003.
PA Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 47
ID ADC12109 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003049681-A1.
PD 13-MAR-2003.
PA Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 48
ID ADC56531 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003064375-A1.
PD 03-APR-2003.
PA Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 49
ID ADC07586 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003068647-A1.
PD 10-APR-2003.
PA Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 50
ID ADC11576 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003068403-A1.
PD 10-APR-2003.
PA Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 51
ID ADC36826 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 52
ID ADC21816 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 53
ID ADC49847 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 54
ID ADC49046 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.

PN US2003088070-A1.
PD 08-MAY-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 55
ID ADC49563 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 56
ID ADC47424 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 57
ID ADC44698 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 58
ID ADC47169 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 59
ID ADD08230 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 60
ID ADC82055 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 61
ID ADD07697 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 62
ID ADC78044 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 63
ID ADC82588 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;

RESULT 64
ID ADD06279 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 65
ID ADD08768 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 66
ID ADC77798 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 67
ID ADD07017 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2002193100-A1.
PD 19-DEC-2002.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 68
ID ADC83264 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 69
ID ADD50761 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 70
ID ADD51007 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GENTECH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 71
ID ADD55371 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003077553-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 72
ID ADD56329 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 73
ID ADD50488 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096971-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 74
ID ADD54767 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2002132253-A1.
PD 19-FEB-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 75
ID ADD50242 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 76
ID ADD51253 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 77
ID ADE26921 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 78
ID ADE26388 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 79
ID ADF67325 standard; cDNA; 907 BP.
DE Human PRO1187 nucleotide sequence SEQ ID NO:398.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 80
ID ADI35579 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 81
ID ADI00072 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003045682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 82
ID ABX77968 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 83
ID AC669286 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.

PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 84
ID ABX90357 standard; cDNA; 907 BP.
DE Human secreted/transmembrane protein cDNA, #160.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 85
ID ACA66889 standard; cDNA; 907 BP.
DE cDNA encoding human PRO polypeptide #49.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 86
ID ACD66641 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 87
ID ABX64203 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 88
ID ADC46800 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 89
ID ADE20971 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 90
ID ADE05815 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 91
ID ADD75044 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 92
ID ADD75790 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 93
ID ADD85022 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 94
ID ADD86848 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 95
ID ADE20725 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 96
ID ADE39022 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 97
ID ADE05569 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 98
ID ADD73554 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 99
ID ADD78394 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 100
ID ADE21217 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 101
ID ADD77332 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 102
ID ADE20479 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 103
ID ADD75544 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100654-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 104
ID ADD74060 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 105
ID ADD74306 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 106
ID ADD76036 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 107
ID ADD85528 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 108
ID ADE05077 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 109
ID ADD75290 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 110
ID ADD76834 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 111
ID ADD76834 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
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Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 111
ID ADD86602 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 112
ID ADD78070 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 113
ID ADD77578 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 114
ID ADD77824 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 115
ID ADD85282 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 116
ID ADD73814 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 117
ID ADD74552 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 118
ID ADD77080 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 119
ID ADD85774 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 120
ID AD805323 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 121
ID ADD74798 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 122
ID ADF35524 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 123
ID ADG11774 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 124
ID ADG05610 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 125
ID ADG27164 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 126
ID ADG11227 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 127
ID ADG12006 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 128
ID ADP94563 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 129
ID ADG06659 standard; cDNA; 907 BP.
```


DE Human PRO polynucleotide #49.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 130
ID ADH39003 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 131
ID ADH19644 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 132
ID ADH21137 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 133
ID ADH20177 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 134
ID ADG34093 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 135
ID ADI33563 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 136
ID ADH69657 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 137
ID ADI29818 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 138
ID ADM7215 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2004044179-A1.

PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 139
ID ADK66573 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 140
ID ABK42709 standard; DNA; 17761 BP.
DE Genomic sequence #608 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 907; DB 4; Length 17761;
Best Local Similarity 100.0%; Pred. No. 8.3e-250;
RESULT 141
ID AAK79415 standard; DNA; 17761 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:34227.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 907; DB 4; Length 17761;
Best Local Similarity 100.0%; Pred. No. 8.3e-250;
RESULT 142
ID ADB60865 standard; DNA; 17761 BP.
DE Connective tissue related genomic DNA #608.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 907; DB 9; Length 17761;
Best Local Similarity 100.0%; Pred. No. 8.3e-250;
RESULT 143
ID ABZ11322 standard; cDNA; 1154 BP.
DE Human polynucleotide SEQ ID NO 204.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 66.3%; Score 601.6; DB 6; Length 1154;
Best Local Similarity 99.3%; Pred. No. 2e-162;
RESULT 144
ID ADM43840 standard; cDNA; 1154 BP.
DE Novel human arginine-rich protein cDNA #204.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (KURA/) XUE A.
PA (DRMA/) DRMANC R T.
Query Match 66.3%; Score 601.6; DB 12; Length 1154;
Best Local Similarity 99.3%; Pred. No. 2e-162;
RESULT 145
ID AAF60563 standard; cDNA; 500 BP.
DE Receptor #51 partial coding sequence.
PN US6183968-B1.
PD 06-FEB-2001.
PA (INCY-) INCYTE PHARM INC.
Query Match 55.1%; Score 500; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.4e-133;
RESULT 146
ID ABL62546 standard; cDNA; 480 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:5524.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 50.5%; Score 458; DB 6; Length 480;
Best Local Similarity 99.6%; Pred. No. 2.9e-121;
RESULT 147
ID ABL60189 standard; cDNA; 425 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:3167.

PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 44.4%; Score 403; DB 6; Length 425;
Best Local Similarity 99.5%; Pred. No. 1.8e-105;
RESULT 148
ID ABL80621 standard; cDNA; 402 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:3599.
DN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 40.7%; Score 369; DB 6; Length 402;
Best Local Similarity 99.3%; Pred. No. 1.1e-95;
RESULT 149
ID ABL8135 standard; cDNA; 360 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:6113.
DN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 37.9%; Score 344.2; DB 6; Length 360;
Best Local Similarity 98.9%; Pred. No. 1.4e-88;
RESULT 150
ID AAF66312 standard; cDNA; 399 BP.
DE Novel human polynucleotide, SEQ ID NO: 2068.
DN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSRO INC.
Query Match 24.6%; Score 222.8; DB 5; Length 399;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
RESULT 151
ID AAF6311 standard; cDNA; 395 BP.
DE Novel human polynucleotide, SEQ ID NO: 2067.
DN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSRO INC.
Query Match 23.8%; Score 215.6; DB 5; Length 395;
Best Local Similarity 98.2%; Pred. No. 1.4e-51;
RESULT 152
ID AAS35690 standard; DNA; 10093 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1390.
DN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.5%; Score 213; DB 4; Length 10093;
Best Local Similarity 85.8%; Pred. No. 2.7e-50;
RESULT 153
ID ABA07184 standard; DNA; 10093 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.
DN WO200155306-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.5%; Score 213; DB 4; Length 10093;
Best Local Similarity 85.8%; Pred. No. 2.7e-50;
RESULT 154
ID AAK89616 standard; DNA; 10093 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3392.
DN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.5%; Score 213; DB 4; Length 10093;
Best Local Similarity 85.8%; Pred. No. 2.7e-50;
RESULT 155
ID ADB46584 standard; DNA; 10093 BP.
DE Human cardiovascular system related genomic DNA #150.
DN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.5%; Score 213; DB 10; Length 10093;
Best Local Similarity 85.8%; Pred. No. 2.7e-50;
RESULT 156
ID ADJ08002 standard; DNA; 10093 BP.

DE Human cardiovascular system associated polypeptide-related DNA SeqID1390.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.5%; Score 213; DB 13; Length 10093;
Best Local Similarity 85.8%; Pred. No. 2.7e-50;
RESULT 157
ID AAL04218 standard; DNA; 32148 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6906.
DN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.5%; Score 212.8; DB 4; Length 32148;
Best Local Similarity 83.8%; Pred. No. 4.8e-50;
RESULT 158
ID AAS36445 standard; DNA; 17397 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1945.
DN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 4; Length 17397;
Best Local Similarity 73.6%; Pred. No. 5.7e-50;
RESULT 159
ID ADB47139 standard; DNA; 17397 BP.
DE Human cardiovascular system related genomic DNA #705.
DN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 10; Length 17397;
Best Local Similarity 73.6%; Pred. No. 5.7e-50;
RESULT 160
ID ADJ08557 standard; DNA; 17397 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1945.
DN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 13; Length 17397;
Best Local Similarity 73.6%; Pred. No. 5.7e-50;
RESULT 161
ID AAS36443 standard; DNA; 19334 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1943.
DN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 4; Length 19334;
Best Local Similarity 73.6%; Pred. No. 5.9e-50;
RESULT 162
ID ADB47137 standard; DNA; 19334 BP.
DE Human cardiovascular system related genomic DNA #703.
DN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 10; Length 19334;
Best Local Similarity 73.6%; Pred. No. 5.9e-50;
RESULT 163
ID ADJ08555 standard; DNA; 19334 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1943.
DN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 13; Length 19334;
Best Local Similarity 73.6%; Pred. No. 5.9e-50;
RESULT 164
ID AAS36444 standard; DNA; 19345 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1944.
DN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.4%; Score 212.2; DB 4; Length 19345;
Best Local Similarity 73.6%; Pred. No. 5.9e-50;
RESULT 165
ID ADB47138 standard; DNA; 19345 BP.
DE Human cardiovascular system related genomic DNA #704.

PN US2003059908-A1.
PD 27-MAR-2003.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.4%; Score 212.2; DB 10; Length 19345;
Best Local Similarity 73.6%; Pred. No. 5.9e-50;
RESULT 166
ID ADJ08556 standard; DNA; 19345 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1944.
PN US2004005575-A1.
PD 08-JUN-2004.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.4%; Score 212.2; DB 13; Length 19345;
Best Local Similarity 73.6%; Pred. No. 5.9e-50;
RESULT 167
ID AD085575 standard; DNA; 29001 BP.
DE Human zinedin polynucleotide.
PN US2004110701-A1.
PD 10-JUN-2004.
Query Match (ISIS-) ISIS PHARM INC. 23.4%; Score 212.2; DB 12; Length 29001;
Best Local Similarity 73.6%; Pred. No. 6.9e-50;
RESULT 168
ID ACN44806 standard; DNA; 177587 BP.
DE Human genomic sequence hCG40093.
PN WO2003073826-A2.
PD 12-SEP-2003.
Query Match (SAGRE-) SAGRES DISCOVERY. 23.4%; Score 211.8; DB 11; Length 177587;
Best Local Similarity 84.0%; Pred. No. 1.8e-49;
RESULT 169
ID ACN44586 standard; DNA; 118931 BP.
DE Human genomic sequence hCG30014.
PN WO2003073826-A2.
PD 12-SEP-2003.
Query Match (SAGRE-) SAGRES DISCOVERY. 23.3%; Score 211.6; DB 11; Length 118931;
Best Local Similarity 86.0%; Pred. No. 1.8e-49;
RESULT 170
ID AAK93310 standard; DNA; 24664 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4886.
PN WO200155314-A2.
PD 02-AUG-2001.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.3%; Score 211.2; DB 4; Length 24664;
Best Local Similarity 83.8%; Pred. No. 1.3e-49;
RESULT 171
ID AAS32137 standard; DNA; 24664 BP.
DE Human liver associated genomic DNA #311.
PN WO200155355-A1.
PD 02-AUG-2001.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.3%; Score 211.2; DB 6; Length 24664;
Best Local Similarity 83.8%; Pred. No. 1.3e-49;
RESULT 172
ID ABN90492 standard; DNA; 24664 BP.
DE Human liver antigen HPV1084 genomic sequence, SEQ ID NO: 613.
PN US2002042096-A1.
PD 11-APR-2002.
Query Match (ROSE/) ROSEN C A. 23.1%; Score 209.4; DB 5; Length 19616;
PA (RUBE/) RUBEN S M. 23.1%; Score 209.4; DB 5; Length 19616;
PA (BARA/) BARASH S C. 23.1%; Score 209.4; DB 5; Length 19616;
Query Match Best Local Similarity 83.8%; Pred. No. 1.3e-49;
RESULT 173
ID ADJ15405 standard; DNA; 24664 BP.
DE Human liver-related genomic DNA - SEQ ID 613.
PN US2003077602-A1.
PD 24-APR-2003.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.3%; Score 211.2; DB 11; Length 24664;
Best Local Similarity 83.8%; Pred. No. 1.3e-49;
RESULT 174
ID ADP13332 standard; DNA; 126990 BP.
DE Renal cell carcinoma differentially expressed gene #68.
PN WO2004048933-A2.
PD 10-JUN-2004.
Query Match (AMHP) WYETH. 23.2%; Score 210.6; DB 12; Length 126990;
Best Local Similarity 80.2%; Pred. No. 3.5e-49;
RESULT 175
ID ADH59595 standard; DNA; 301 BP.
DE Alu-repeat consensus sequence #1.
PN WO2003027328-A2.
PD 03-APR-2003.
Query Match (BOST-) BOSTON PROBES INC. 23.2%; Score 210; DB 10; Length 301;
PA (DAKO-) DAKOCYTOMATION DENMARK AS. 23.2%; Score 210; DB 10; Length 301;
Query Match Best Local Similarity 86.8%; Pred. No. 5.1e-50;
RESULT 176
ID AAK79904 standard; DNA; 2744 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34716.
PN WO200157182-A2.
PD 09-AUG-2001.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.1%; Score 209.8; DB 4; Length 2744;
Best Local Similarity 82.6%; Pred. No. 1.4e-49;
RESULT 177
ID AAF97846 standard; DNA; 51474 BP.
DE Human neuroblastoma cell line NB-1 ip36 nucleotide sequence SEQ ID NO:60.
PN WO200116311-A1.
PD 08-MAR-2001.
Query Match (HISM) HISAMITSU PHARM CO LTD. 23.1%; Score 209.8; DB 5; Length 51474;
PA (CHIB-) CHIBA PREPCTURE. 23.1%; Score 209.8; DB 5; Length 51474;
Query Match Best Local Similarity 82.8%; Pred. No. 4.2e-49;
RESULT 178
ID ABR83565 standard; cDNA; 122888 BP.
DE Human cDNA differentially expressed in granulocytic cells #140.
PN WO200228999-A2.
PD 11-APR-2002.
Query Match (GENE-) GENE LOGIC INC. 23.1%; Score 209.8; DB 6; Length 122888;
Best Local Similarity 85.1%; Pred. No. 5.9e-49;
RESULT 179
ID AAL36855 standard; DNA; 19616 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3220.
PN WO200155367-A1.
PD 02-AUG-2001.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.1%; Score 209.4; DB 4; Length 19616;
Best Local Similarity 86.7%; Pred. No. 3.8e-49;
RESULT 180
ID ABA16856 standard; DNA; 19616 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9187.
PN WO200159063-A2.
PD 16-AUG-2001.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.1%; Score 209.4; DB 5; Length 19616;
Best Local Similarity 86.7%; Pred. No. 3.8e-49;
RESULT 181
ID ABA16094 standard; DNA; 19616 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8425.
PN WO200159063-A2.
PD 16-AUG-2001.
Query Match (HUMA-) HUMAN GENOME SCI INC. 23.1%; Score 209.4; DB 5; Length 19616;
Best Local Similarity 86.7%; Pred. No. 3.8e-49;
RESULT 182
ID ABX59843 standard; cDNA; 19616 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2187.

PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 23.1%; Score 209.4; DB 8; Length 19616;
 Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 RESULT 183
 ID ADJ30593 standard; DNA; 19616 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3220.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.4; DB 12; Length 19616;
 Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 RESULT 184
 ID AAI62651 standard; DNA; 614 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 301.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 614;
 Best Local Similarity 83.3%; Pred. No. 1.1e-49;
 RESULT 185
 ID AAI06745 standard; DNA; 614 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9433.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 614;
 Best Local Similarity 83.3%; Pred. No. 1.1e-49;
 RESULT 186
 ID AAI62649 standard; DNA; 691 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 299.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 691;
 Best Local Similarity 83.3%; Pred. No. 1.2e-49;
 RESULT 187
 ID AAI06743 standard; DNA; 691 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9431.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 691;
 Best Local Similarity 83.3%; Pred. No. 1.2e-49;
 RESULT 188
 ID AAI62650 standard; DNA; 16225 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 300.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 189
 ID AAK81913 standard; DNA; 16225 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36725.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 190
 ID AAI06744 standard; DNA; 16225 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9432.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 191
 ID AAS30106 standard; DNA; 16225 BP.

DE Human lung antigen genomic DNA #176.
 PN WO200155303-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 5; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 192
 ID ADB33443 standard; DNA; 16225 BP.
 DE Human novel lung related polypeptide DNA SEQ ID NO 370.
 PN US2003054368-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 10; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 193
 ID ADA43380 standard; cDNA; 50000 BP.
 DE Human asthma associated gene, AAGB, genomic fragment #1.
 PN US2003104521-A1.
 PD 05-JUN-2003.
 PA (WHIT/) WHITTAKER P A.
 Query Match 23.1%; Score 209.2; DB 6; Length 50000;
 Best Local Similarity 82.5%; Pred. No. 6.2e-49;
 RESULT 194
 ID ABA98944 standard; DNA; 50000 BP.
 DE Human asthma-associated gene AAGB genomic DNA #1.
 PN WO200206312-A2.
 PD 24-JAN-2002.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 Query Match 23.1%; Score 209.2; DB 6; Length 50000;
 Best Local Similarity 82.5%; Pred. No. 6.2e-49;
 RESULT 195
 ID ABL42416 standard; DNA; 59065 BP.
 DE Human serine/threonine kinase DNA.
 PN US6340583-B1.
 PD 22-JAN-2002.
 PA (PEKE) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 6; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 196
 ID AAD41839 standard; DNA; 59065 BP.
 DE Human LIM domain kinase (LIMK) gene.
 PN US6403353-B1.
 PD 11-JUN-2002.
 PA (PEKE) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 6; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 197
 ID ADG98727 standard; DNA; 59065 BP.
 DE Human kinase genomic DNA.
 PN US2003166215-A1.
 PD 04-SEP-2003.
 PA (PEKE) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 10; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 198
 ID ADR44808 standard; DNA; 59065 BP.
 DE Human kinase genomic DNA.
 PN US2004175751-A1.
 PD 09-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 23.1%; Score 209.2; DB 13; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 199
 ID ABK83459 standard; cDNA; 128978 BP.
 DE Human cDNA differentially expressed in granulocytic cells #30.
 PN WO200228899-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 23.1%; Score 209.2; DB 6; Length 128978;
 Best Local Similarity 79.7%; Pred. No. 9e-49;
 RESULT 200
 ID AAD54587 standard; DNA; 128978 BP.

DE Human LTM kinase (LIMK) DNA #6.
PN WO200299048-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 23.1%; Score 209.2; DB 8; Length 128978;
Best Local Similarity 79.7%; Pred. No. 9e-49;
RESULT 201
ID ADS2994 standard; DNA; 128978 BP.
DE Drug therapy altered expressed gene #345.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) MYETH.
PA (BURE/) BURCZYNSKI M.
PA (TWIN/) TWINE N. J.
PA (DORN/) DORNER A. J.
PA (TREE/) TREPTICHO W. L.
Query Match 23.1%; Score 209.2; DB 13; Length 128978;
Best Local Similarity 79.7%; Pred. No. 9e-49;
RESULT 202
Query Match 23.0%; Score 209; DB 11; Length 110000;
Best Local Similarity 84.4%; Pred. No. 9.6e-49;
RESULT 203
ID ADQ18757 standard; DNA; 43712 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1576.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 23.0%; Score 208.8; DB 12; Length 43712;
Best Local Similarity 82.7%; Pred. No. 7.7e-49;
RESULT 204
ID ADQ97727 standard; DNA; 73063 BP.
DE Human cancer associated sequence H010-034, SEQ ID 704.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 23.0%; Score 208.8; DB 12; Length 73063;
Best Local Similarity 85.1%; Pred. No. 9.4e-49;
RESULT 205
ID ABAK2912 standard; DNA; 518 BP.
DE Genomic sequence #811 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 208.6; DB 4; Length 518;
Best Local Similarity 83.6%; Pred. No. 1.6e-49;
RESULT 206
ID ADB61068 standard; DNA; 518 BP.
DE Connective tissue related genomic DNA #811.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 208.6; DB 9; Length 518;
Best Local Similarity 83.6%; Pred. No. 1.6e-49;
RESULT 207
ID ADE82948 standard; DNA; 167163 BP.
DE Human PYT1 genomic DNA sequence.
PN WO2003060808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 23.0%; Score 208.6; DB 10; Length 167163;
Best Local Similarity 84.6%; Pred. No. 1.5e-48;
RESULT 208
ID AAK79905 standard; DNA; 2744 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34717.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 208.2; DB 4; Length 2744;
Best Local Similarity 82.3%; Pred. No. 4e-49;
RESULT 209
ID ADN06353 standard; DNA; 398800 BP.
DE Human FLAP genomic DNA SEQ ID NO:1.
PN WO2004035741-A2.

PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 23.0%; Score 208.2; DB 12; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.6e-48;
RESULT 210
ID ADS94372 standard; DNA; 398800 BP.
DE Human 5-lipoxygenase activating protein (FLAP) gene.
PN WO2004035746-A2.
PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 23.0%; Score 208.2; DB 13; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.6e-48;
RESULT 211
ID ABL69793 standard; DNA; 291 BP.
DE Prostate cancer related gene sequence SEQ ID NO:8130.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.9%; Score 208; DB 6; Length 291;
Best Local Similarity 87.2%; Pred. No. 1.9e-49;
RESULT 212
ID ABL67475 standard; DNA; 291 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5812.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.9%; Score 208; DB 6; Length 291;
Best Local Similarity 87.2%; Pred. No. 1.9e-49;
RESULT 213
ID ADP65796 standard; DNA; 270150 BP.
DE Human 16P13 sequence section 7 of 8 DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 22.9%; Score 208; DB 11; Length 270150;
Best Local Similarity 79.2%; Pred. No. 2.6e-48;
RESULT 214
ID AAK71190 standard; DNA; 3139 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26002.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.9%; Score 207.8; DB 4; Length 3139;
Best Local Similarity 78.7%; Pred. No. 5.4e-49;
RESULT 215
ID ADQ20461 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.9%; Score 207.8; DB 12; Length 166181;
Best Local Similarity 85.0%; Pred. No. 2.5e-48;
RESULT 216
ID ADQ18633 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.9%; Score 207.8; DB 12; Length 166181;
Best Local Similarity 85.0%; Pred. No. 2.5e-48;
RESULT 217
ID AAD22781 standard; DNA; 31766 BP.
DE Human sulphate transporter protein splice form genomic DNA.
PN WO200181412-A2.
PD 01-NOV-2001.
PA (PEKE) PE CORP NY.
Query Match 22.9%; Score 207.6; DB 6; Length 31766;
Best Local Similarity 85.8%; Pred. No. 1.5e-48;
RESULT 218
ID AAL50687 standard; DNA; 31766 BP.
DE Human sulphate transporter protein genomic DNA sequence.
PN WO200259306-A2.
PD 01-AUG-2002.

PA (APPL-) APPLERA CORP. 22.9%; Score 207.6; DB 6; Length 31766;
Query Match
Best Local Similarity 85.8%; Pred. No. 1.5e-48;
RESULT 219
ID ABR84242 standard; cDNA; 43599 BP.
DE Human cDNA differentially expressed in granulocytic cells #813.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.9%; Score 207.4; DB 6; Length 43599;
Best Local Similarity 84.0%; Pred. No. 1.9e-48;
RESULT 220
ID ADE11169 standard; DNA; 394191 BP.
DE Human transporter protein encoding gene SEQ ID NO:1.
Query Match 22.8%; Score 207.2; DB 10; Length 110000;
Best Local Similarity 86.3%; Pred. No. 3.2e-48;
RESULT 221
ID ABA16169 standard; DNA; 4969 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8500.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.8%; Score 207; DB 5; Length 4969;
Best Local Similarity 84.2%; Pred. No. 1.1e-48;
RESULT 222
ID ABR83502 standard; cDNA; 77425 BP.
DE Human cDNA differentially expressed in granulocytic cells #73.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.8%; Score 206.8; DB 6; Length 77425;
Best Local Similarity 86.3%; Pred. No. 3.6e-48;
RESULT 223
ID ADQ59434 standard; DNA; 169659 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:70.
PN WO200405828-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.8%; Score 206.8; DB 12; Length 169659;
Best Local Similarity 79.4%; Pred. No. 4.9e-48;
RESULT 224
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.8%; Score 206.6; DB 12; Length 178024;
Best Local Similarity 82.0%; Pred. No. 5.7e-48;
RESULT 225
ID ADQ2756 standard; DNA; 96594 BP.
DE Human MOPF carcinoma associated gene, SEQ ID NO:1274.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.8%; Score 206.4; DB 9; Length 96594;
Best Local Similarity 84.0%; Pred. No. 5.1e-48;
RESULT 226
ID ADB72494 standard; DNA; 96594 BP.
DE Human MOPF gene.
PN WO200308583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.8%; Score 206.4; DB 10; Length 96594;
Best Local Similarity 84.0%; Pred. No. 5.1e-48;
RESULT 227
ID ADC85236 standard; DNA; 96594 BP.
DE Human MOPF genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.8%; Score 206.4; DB 10; Length 96594;
Best Local Similarity 84.0%; Pred. No. 5.1e-48;
RESULT 228
ID ADM74351 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #10.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39341.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 4; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 230
ID ADA98945 standard; DNA; 16146 BP.
DE Human secreted protein-related DNA sequence #538.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 8; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 231
ID ADA44551 standard; DNA; 16146 BP.
DE Human secreted protein DNA SEQ ID 744.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 8; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 232
ID ADC20980 standard; DNA; 16146 BP.
DE Human secreted protein-related DNA sequence #398.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 233
ID ADP11004 standard; DNA; 16146 BP.
DE Human secreted protein encoding sequence #326.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 234
ID ABR17011 standard; DNA; 16146 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 365.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 235
ID ABE68089 standard; DNA; 16146 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1612.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 236
ID ACN44482 standard; DNA; 34096 BP.
DE Human genomic sequence hCG26017.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 206.2; DB 11; Length 34096;
Best Local Similarity 78.4%; Pred. No. 3.9e-48;
RESULT 237

ID AAF58067 standard; DNA; 39198 BP.
DE Human polyamine-modulated factor-1 PMF-1 gene.
PN WO200107610-A1.
PD 01-FEB-2001.
PA (UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 22.7%; Score 206.2; DB 5; Length 39198;
Best Local Similarity 84.7%; Pred. No. 4.1e-48;
RESULT 238
ID ABB95533 standard; DNA; 48436 BP.
DE Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
PN US2002061562-A1.
PD 23-MAY-2002.
PA (FUKU) FUKUDA M N.
Query Match 22.7%; Score 206.2; DB 6; Length 48436;
Best Local Similarity 79.9%; Pred. No. 4.5e-48;
RESULT 239
ID ADL13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO200305416-A2.
PD 03-JUL-2003.
PA (INCYT) INCYTE GENOMICS INC.
Query Match 22.7%; Score 206.2; DB 10; Length 167932;
Best Local Similarity 84.7%; Pred. No. 7.2e-48;
RESULT 240
ID ABB97883 standard; DNA; 50849 BP.
DE Human glutathione reductase (GSR) gene SEQ ID NO:1.
PN WO200242320-A2.
PD 30-MAY-2002.
PA (GENA-) GENAMISSANCE PHARM INC.
Query Match 22.7%; Score 206; DB 6; Length 50849;
Best Local Similarity 81.7%; Pred. No. 5.2e-48;
RESULT 241
ID ADQ97152 standard; DNA; 58651 BP.
DE Human cancer associated sequence HD08-008, SEQ ID NO:128.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.7%; Score 206; DB 12; Length 58651;
Best Local Similarity 79.0%; Pred. No. 5.5e-48;
RESULT 242
Query Match 22.7%; Score 206; DB 12; Length 87411;
Best Local Similarity 84.4%; Pred. No. 6.4e-48;
RESULT 243
ID ABA16120 standard; DNA; 447 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8451.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 5; Length 447;
Best Local Similarity 84.9%; Pred. No. 9.6e-49;
RESULT 244
ID ABA20765 standard; DNA; 447 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13096.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 5; Length 447;
Best Local Similarity 84.9%; Pred. No. 9.6e-49;
RESULT 245
ID AAK67925 standard; DNA; 451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22737.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 4; Length 451;
Best Local Similarity 84.9%; Pred. No. 9.7e-49;
RESULT 246
ID AAK81748 standard; DNA; 451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36560.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.7%; Score 205.8; DB 4; Length 451;
Best Local Similarity 84.9%; Pred. No. 9.7e-49;
RESULT 247
ID ABA16121 standard; DNA; 451 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8452.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 5; Length 451;
Best Local Similarity 84.9%; Pred. No. 9.7e-49;
RESULT 248
ID AAQ92779 standard; DNA; 6905 BP.
DE Human thymopoietin continuous gene fragment.
PN WO9517205-A1.
PD 29-JUN-1995.
PA (IMMU-) IMMUNOBIOLOGY RES INST INC.
Query Match 22.7%; Score 205.8; DB 2; Length 6905;
Best Local Similarity 83.6%; Pred. No. 2.8e-48;
RESULT 249
ID ADO19382 standard; DNA; 6905 BP.
DE Human PRO polynucleotide #720.
PN WO200404361-A2.
PD 27-MAY-2004.
PA (GENTH) GENTECH INC.
Query Match 22.7%; Score 205.8; DB 12; Length 6905;
Best Local Similarity 83.6%; Pred. No. 2.8e-48;
RESULT 250
ID ACN37228 standard; DNA; 32640 BP.
DE Human periodontal disease related gene KRT23 SEQ ID NO:138.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
Query Match 22.7%; Score 205.8; DB 13; Length 32640;
Best Local Similarity 82.4%; Pred. No. 5e-48;
RESULT 251
ID ACN43878 standard; DNA; 39148 BP.
DE Human genomic sequence hCG36720.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 11; Length 39148;
Best Local Similarity 83.6%; Pred. No. 5.4e-48;
RESULT 252
ID ADA02696 standard; DNA; 59554 BP.
DE Human TK2 carcinoma associated gene, SEQ ID NO:1214.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 9; Length 59554;
Best Local Similarity 86.3%; Pred. No. 6.3e-48;
RESULT 253
ID ADB72434 standard; DNA; 59554 BP.
DE Human TK2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 10; Length 59554;
Best Local Similarity 86.3%; Pred. No. 6.3e-48;
RESULT 254
ID ADB95944 standard; DNA; 59554 BP.
DE Human TK2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 10; Length 59554;
Best Local Similarity 86.3%; Pred. No. 6.3e-48;
RESULT 255
ID ABA16034 standard; DNA; 203654 BP.
DE Human gene encoding calcium channel transporter family member.
PN US2002142938-A1.
PD 03-OCT-2002.
PA (YANC/) YAN C.

PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 22.7%; Score 205.8; DB 10; Length 203654;
Best Local Similarity 82.7%; Pred. No. 1e-47;
RESULT 256
ID AAS42054 standard; DNA; 10085 BP.
DE Genomic sequence #370 encoding novel human enzyme polypeptide.
PN W0200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.6; DB 4; Length 10085;
Best Local Similarity 81.7%; Pred. No. 3.6e-48;
RESULT 257
ID AAL02803 standard; DNA; 10085 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5491.
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.6; DB 4; Length 10085;
Best Local Similarity 81.7%; Pred. No. 3.6e-48;
RESULT 258
ID AAD54634 standard; DNA; 142519 BP.
DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
PN W0200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 22.7%; Score 205.6; DB 10; Length 142519;
Best Local Similarity 84.4%; Pred. No. 1e-47;
RESULT 259
ID AAS23041 standard; DNA; 719 BP.
DE DNA encoding novel bone marrow polypeptide #135.
PN W0200157187-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.6%; Score 205.4; DB 4; Length 719;
Best Local Similarity 85.2%; Pred. No. 1.5e-48;
RESULT 260
ID ABO72698 standard; cDNA; 2619 BP.
DE Human MDR1 encoding cDNA SEQ ID NO 250.
PN W0200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.6%; Score 205.4; DB 6; Length 2619;
Best Local Similarity 82.6%; Pred. No. 2.5e-48;
RESULT 261
ID AAK84729 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39541.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48037;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 262
ID AAK85983 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40795.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48037;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 263
ID AAK84730 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39542.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48045;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 264
ID AAK85984 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796.
PN W0200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.4; DB 4; Length 48045;
Best Local Similarity 86.5%; Pred. No. 7.6e-48;
RESULT 265
ID AAZ00870 standard; DNA; 56516 BP.
DE PGI genomic coding sequence.
PN W0932644-A2.
PD 01-JUL-1999.
PA (GEST-) GENSET.
Query Match 22.6%; Score 205.4; DB 2; Length 56516;
Best Local Similarity 78.8%; Pred. No. 8.1e-48;
RESULT 266
ID AAZ01022 standard; DNA; 56520 BP.
DE Wild type Pgi coding sequence.
PN W0932644-A2.
PD 01-JUL-1999.
PA (GEST-) GENSET.
Query Match 22.6%; Score 205.4; DB 2; Length 56520;
Best Local Similarity 78.8%; Pred. No. 8.1e-48;
RESULT 267
ID ADC85367 standard; DNA; 96593 BP.
DE Mouse Bim coding sequence.
PN W02003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 205.4; DB 10; Length 96593;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 268
ID ADA02888 standard; DNA; 96594 BP.
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
PN W02003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 205.4; DB 9; Length 96594;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 269
ID ADB72626 standard; DNA; 96594 BP.
DE Human BLM gene.
PN W02003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 205.4; DB 10; Length 96594;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 270
ID ADM74483 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR-) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 22.6%; Score 205.4; DB 12; Length 96594;
Best Local Similarity 83.9%; Pred. No. 9.9e-48;
RESULT 271
ID ADH59596 standard; DNA; 301 BP.
DE ALU-repeat consensus sequence #2.
PN W02003027328-A2.
PD 03-APR-2003.
PA (BOST-) BOSTON PROBES INC.
PA (DAKO-) DAKOCYTOMATION DENMARK AS.
Query Match 22.6%; Score 205.2; DB 10; Length 301;
Best Local Similarity 85.8%; Pred. No. 1.2e-48;
RESULT 272
ID AAL52585 standard; cDNA; 3673 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 3.
PN W02003102149-A2.
PD 11-DEC-2003.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3673;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 273
ID AAL52588 standard; cDNA; 3673 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 9.

PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3673;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 274
ID AAL52584 standard; cDNA; 3674 BP.
DE Human BHD coding sequence.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3674;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 275
ID AAL52589 standard; cDNA; 3674 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 11.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3674;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 276
ID AAL52587 standard; cDNA; 3675 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 7.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3675;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 277
ID AAL52618 standard; DNA; 3676 BP.
DE Human BHD consensus sequence.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3676;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 278
ID AAL52586 standard; cDNA; 3702 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 5.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3702;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 279
ID AAK80061 standard; DNA; 5279 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34873.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.2; DB 4; Length 5279;
Best Local Similarity 83.4%; Pred. No. 3.7e-48;
RESULT 280
ID AAK80062 standard; DNA; 5279 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34874.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.2; DB 4; Length 5279;
Best Local Similarity 83.4%; Pred. No. 3.7e-48;
RESULT 281
ID AAK80060 standard; DNA; 5279 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34872.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.2; DB 4; Length 5279;
Best Local Similarity 83.4%; Pred. No. 3.7e-48;
RESULT 282
ID AAZ60888 standard; DNA; 17131 BP.
DE DNA encoding a human geranylgeranyl pyrophosphate synthetase (hGGPPS).
PN WO200005382-A2.

PD 03-FEB-2000.
PA (GEST) GENSET.
Query Match 22.6%; Score 205.2; DB 3; Length 17131;
Best Local Similarity 83.3%; Pred. No. 5.8e-48;
RESULT 283
ID AAA35185 standard; DNA; 32351 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:59.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 284
ID AAP21307 standard; DNA; 32351 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2874.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 285
ID AB297001 standard; DNA; 32351 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 10; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 286
ID ABD20850 standard; DNA; 32351 BP.
DE Human pulmonary and inflammatory target DNA #461.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 11; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 287
ID AAA35169 standard; DNA; 40298 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:63.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 288
ID AAF21311 standard; DNA; 40298 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2878.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 289
ID AB297005 standard; DNA; 40298 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 10; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 290
ID ABD20854 standard; DNA; 40298 BP.
DE Human pulmonary and inflammatory target DNA #465.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 11; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 291
ID ADJ10262 standard; DNA; 51001 BP.
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA segid 11.

PN US2004005570-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 12; Length 51001;
Best Local Similarity 83.3%; Pred. No. 8.9e-48;
RESULT 292
ID ADL13556 standard; DNA; 95240 BP.
DE Osteoarthritis-associated polymorphic nucleotide #88.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.6%; Score 205.2; DB 10; Length 95240;
Best Local Similarity 84.7%; Pred. No. 1.1e-47;
RESULT 293
ID ABK83497 standard; cDNA; 227968 BP.
DE Human cDNA differentially expressed in granulocytic cells #68.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.6%; Score 205; DB 6; Length 227968;
Best Local Similarity 84.1%; Pred. No. 1.8e-47;
RESULT 294
ID ADL18538 standard; DNA; 227968 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.6%; Score 205; DB 12; Length 227968;
Best Local Similarity 84.1%; Pred. No. 1.8e-47;
RESULT 295
ID AAQ93781 standard; DNA; 3234 BP.
DE Human thymopolein gene fragment.
PN WO9517205-A1.
PD 29-JUN-1995.
PA (IMMU-) IMMUNOBIOLOGY RES. INST INC.
Query Match 22.6%; Score 204.8; DB 2; Length 3234;
Best Local Similarity 76.5%; Pred. No. 4e-48;
RESULT 296
ID AAS41738 standard; DNA; 32217 BP.
DE Genomic sequence #54 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.8; DB 4; Length 32217;
Best Local Similarity 79.6%; Pred. No. 9.7e-48;
RESULT 297
ID ADL10262 standard; DNA; 51001 BP.
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
PN US2004005570-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.6%; Score 204.8; DB 12; Length 51001;
Best Local Similarity 77.1%; Pred. No. 1.2e-47;
RESULT 298
ID ADC87336 standard; DNA; 108316 BP.
DE Human GPCR gene SEQ ID NO:1789.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
DE (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
PN WO2004005570-A1.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.6; DB 4; Length 16997;
Best Local Similarity 81.8%; Pred. No. 8.7e-48;
RESULT 299
ID ADL13556 standard; DNA; 95240 BP.
DE Osteoarthritis-associated polymorphic nucleotide #88.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.6%; Score 205.2; DB 10; Length 95240;
Best Local Similarity 84.7%; Pred. No. 1.1e-47;
RESULT 300
ID AAK86146 standard; DNA; 16997 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40958.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.6; DB 4; Length 16997;
Best Local Similarity 81.8%; Pred. No. 8.7e-48;
RESULT 301
ID AAK80033 standard; DNA; 16997 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34845.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.6; DB 4; Length 16997;
Best Local Similarity 81.8%; Pred. No. 8.7e-48;
RESULT 302
ID ACN44998 standard; DNA; 122614 BP.
DE Human genomic sequence hCG29191.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 204.6; DB 11; Length 122614;
Best Local Similarity 83.2%; Pred. No. 1.9e-47;
RESULT 303
ID ADL08109 standard; DNA; 247682 BP.
DE Human gene associated with low HDL-C AT3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 22.6%; Score 204.6; DB 12; Length 247682;
Best Local Similarity 81.8%; Pred. No. 2.4e-47;
RESULT 304
ID AAK85292 standard; DNA; 2680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40104.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 2680;
Best Local Similarity 82.7%; Pred. No. 4.9e-48;
RESULT 305
ID AAL45661 standard; DNA; 5970 BP.
DE Mammary gland bioreactor related DNA #2.
PN CN1324952-A.
PD 05-DEC-2001.
PA (ZHON-) ZHONGLU BIOLOGICAL ENG CO LTD SHANGHAI.
Query Match 22.5%; Score 204.4; DB 6; Length 5970;
Best Local Similarity 81.4%; Pred. No. 6.6e-48;
RESULT 306
ID AAA34833 standard; DNA; 6870 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2522.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;
RESULT 307
ID AAP20955 standard; DNA; 6870 BP.
DE Interleukin-11 polynucleotide fragment #2522.
PN WO2000062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 10; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;
RESULT 308
ID ABZ96649 standard; DNA; 6870 BP.
DE Human interleukin-11 nucleic acid.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 10; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;
RESULT 309
ID ABD19514 standard; DNA; 6870 BP.
DE Human interleukin-11 DNA fragment #3.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 11; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;

RESULT 310
ID AAA34834 standard; DNA; 8055 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2523.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 311
ID AAF20956 standard; DNA; 8055 BP.
DE Interleukin-11 polynucleotide fragment #2523.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 312
ID ABZ9650 standard; DNA; 8055 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 10; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 313
ID ABD19512 standard; DNA; 8055 BP.
DE Human Interleukin-11 DNA fragment #1.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 11; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 314
ID AAK87584 standard; DNA; 14417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42396.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 315
ID AAK71816 standard; DNA; 14417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26628.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 316
ID AAK73113 standard; DNA; 14417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27925.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 317
ID AAI62923 standard; DNA; 14417 BP.
DE Human genomic DNA SEQ ID NO 251.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 318
ID ABZ74674 standard; DNA; 14417 BP.
DE Secreted protein gene 391 genomic fragment HB8FC45, SEQ ID NO:1821.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 8; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 319
ID ABZ68196 standard; DNA; 14417 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1719.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 10; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 320
ID AAK73099 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27911.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 321
ID AAK87568 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42380.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 322
ID AAK85290 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40102.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 323
ID AAK71814 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26626.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 324
ID AAI62921 standard; DNA; 14426 BP.
DE Human genomic DNA SEQ ID NO 249.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 325
ID ABZ74673 standard; DNA; 14426 BP.
DE Secreted protein gene 391 genomic fragment HB8FC45, SEQ ID NO:1820.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 8; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 326
ID ABZ68195 standard; DNA; 14426 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1718.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 10; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 327
ID ABD32665 standard; DNA; 112453 BP.
DE Human cancer-associated genomic DNA HD13-070.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.5%; Score 204.4; DB 13; Length 112453;
Best Local Similarity 83.9%; Pred. No. 2e-47;
RESULT 328

ID ADQ59167 standard; DNA; 120670 BP.
 DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:4.
 PN KR2004008012-A.
 PD 28-JAN-2004.
 PA (KIMH/) KIM H G.
 PA (KIMN/) KIM N G.
 PA (LEEJ/) LEE J S.
 PA (RHEB/) RHEB H S.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 12; Length 120670;
 84.1%; Pred. No. 2.1e-47;
 RESULT 329
 ID ADE82948 standard; DNA; 167163 BP.
 DE Human PVT1 genomic DNA sequence.
 PN WO2003080808-A2.
 PD 02-OCT-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 10; Length 167163;
 81.4%; Pred. No. 2.4e-47;
 RESULT 330
 ID AAF21437 standard; DNA; 209273 BP.
 DE Human factor-related antisense polynucleotide #3004.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 3; Length 209273;
 81.4%; Pred. No. 2.6e-47;
 RESULT 331
 ID ABZ97131 standard; DNA; 209274 BP.
 DE Human enzyme-related antisense polynucleotide.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIGENESIS PHARM INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 10; Length 209274;
 81.4%; Pred. No. 2.6e-47;
 RESULT 332
 ID ABD17970 standard; DNA; 209284 BP.
 DE Human factor-related antisense polynucleotide.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIGENESIS PHARM INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 11; Length 209284;
 81.4%; Pred. No. 2.6e-47;
 RESULT 333
 ID ABA96807 standard; CDNA; 1777 BP.
 DE Human uteroglobin 9-encoding CDNA.
 PN WO200198337-A1.
 PD 27-DEC-2001.
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 6; Length 1777;
 80.9%; Pred. No. 4.7e-48;
 RESULT 334
 ID AAC69133 standard; DNA; 4736 BP.
 DE Human ABC1 gene exon 2.
 PN WO200055318-A2.
 PD 21-SEP-2000.
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIOSRESEARCH INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 3; Length 4736;
 80.7%; Pred. No. 6.9e-48;
 RESULT 335
 ID AAS04033 standard; DNA; 11754 BP.
 DE Human ABC1 gene, partial genomic clone #1.
 PN WO200130848-A2.
 PD 03-MAY-2001.
 PA (AVET-) AVENTIS PHARMA SA.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 4; Length 11754;
 80.7%; Pred. No. 9.8e-48;
 RESULT 336
 ID ABL58149 standard; DNA; 11754 BP.
 DE Human ABCA1 transporter gene fragment #3.
 PN WO200236770-A2.
 PD 10-MAY-2002.
 PA (AVET-) AVENTIS PHARMA SA.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 6; Length 11754;
 80.7%; Pred. No. 9.8e-48;
 RESULT 337
 ID ADP65433 standard; DNA; 149034 BP.
 DE Human ABCA1 (ABCA1) gene, complete cde DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 11; Length 149034;
 80.7%; Pred. No. 2.6e-47;
 RESULT 338
 ID AAF92831 standard; DNA; 183999 BP.
 DE Human ABC1 genomic DNA.
 PN WO200115676-A2.
 PD 08-MAR-2001.
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON GENETICS INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 4; Length 183999;
 80.7%; Pred. No. 2.8e-47;
 RESULT 339
 ID AAL04782 standard; DNA; 22927 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7470.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 4; Length 22927;
 81.6%; Pred. No. 1.4e-47;
 RESULT 340
 ID ABL97677 standard; DNA; 22927 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2329.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 4; Length 22927;
 81.6%; Pred. No. 1.4e-47;
 RESULT 341
 ID ADC86460 standard; DNA; 33137 BP.
 DE Human GPCR gene SEQ ID NO: 913.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NRAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 10; Length 33137;
 84.1%; Pred. No. 1.7e-47;
 RESULT 342
 ID ACH03435 standard; DNA; 48840 BP.
 DE Genomic DNA encoding human latrophilin 1 (LPH1).
 PN US2003054347-A1.
 PD 20-MAR-2003.
 PA (UNMI-) UNIV MICHIGAN.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 9; Length 48840;
 84.1%; Pred. No. 1.9e-47;
 RESULT 343
 ID ABR48904 standard; DNA; 3635 BP.
 DE Novel human kallikrein KKL15, Intron 1.
 PN WO200214485-A2.
 PD 21-FEB-2002.
 PA (MOUN-) MOUNT SINAI HOSPITAL.
 Query Match
 Best Local Similarity 22.5%; Score 203.8; DB 6; Length 3635;
 86.2%; Pred. No. 8.1e-48;
 RESULT 344
 ID ABR48346 standard; DNA; 8735 BP.
 DE Genomic DNA encoding novel human kallikrein KKL15.
 PN WO200214485-A2.
 PD 21-FEB-2002.
 PA (MOUN-) MOUNT SINAI HOSPITAL.
 Query Match
 Best Local Similarity 22.5%; Score 203.8; DB 6; Length 8735;
 86.2%; Pred. No. 1.1e-47;
 RESULT 345
 ID ADN10936 standard; DNA; 8735 BP.
 DE Human kallikrein 15 gene, marker of endocrine cancer.

PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 22.5%; Score 203.8; DB 12; Length 8735;
Best Local Similarity 86.2%; Pred. No. 1.1e-47;
RESULT 346
ID ADS36456 standard; DNA; 16640 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1670.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.5%; Score 203.8; DB 13; Length 16640;
Best Local Similarity 86.2%; Pred. No. 1.5e-47;
RESULT 347
ID ADS36479 standard; DNA; 18235 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1693.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.5%; Score 203.8; DB 13; Length 18235;
Best Local Similarity 86.2%; Pred. No. 1.5e-47;
RESULT 348
ID ADA2714 standard; DNA; 53413 BP.
DE Human VDAC1 carcinoma associated gene, SEQ ID NO:1232.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.5%; Score 203.8; DB 9; Length 53413;
Best Local Similarity 79.5%; Pred. No. 2.3e-47;
RESULT 349
ID AD872452 standard; DNA; 53413 BP.
DE Human VDAC1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.5%; Score 203.8; DB 10; Length 53413;
Best Local Similarity 79.5%; Pred. No. 2.3e-47;
RESULT 350
ID AD85962 standard; DNA; 53413 BP.
DE Human VDAC1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.5%; Score 203.8; DB 10; Length 53413;
Best Local Similarity 79.5%; Pred. No. 2.3e-47;
RESULT 351
ID AAD41740 standard; DNA; 99500 BP.
DE Human RECQL2 DNA #1.
PN US6399378-B1.
PD 04-JUN-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.5%; Score 203.8; DB 6; Length 99500;
Best Local Similarity 83.6%; Pred. No. 2.9e-47;
RESULT 352
ID AD133728 standard; DNA; 151212 BP.
DE Osteoarthritis-associated polymorphic nucleotide #260.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.5%; Score 203.8; DB 10; Length 151212;
Best Local Similarity 78.9%; Pred. No. 3.4e-47;
RESULT 353
ID AAK7082 standard; DNA; 4658 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41894.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.6; DB 4; Length 4658;
Best Local Similarity 82.8%; Pred. No. 1e-47;
RESULT 354
ID AB273865 standard; DNA; 18902 BP.
DE Secreted protein gene 71 genomic fragment HCRBF72, SEQ ID NO:1012.
PN WO200277013-A2.

PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.6; DB 8; Length 18902;
Best Local Similarity 81.6%; Pred. No. 1.7e-47;
RESULT 355
ID AB267444 standard; DNA; 18902 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 967.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.6; DB 10; Length 18902;
Best Local Similarity 81.6%; Pred. No. 1.7e-47;
RESULT 356
ID ADD71350 standard; DNA; 93390 BP.
DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.
PN WO2003023063-A1.
PD 20-MAR-2003.
PA (SANY) SANKYO CO LTD.
Query Match 22.4%; Score 203.6; DB 10; Length 93390;
Best Local Similarity 79.8%; Pred. No. 3.2e-47;
RESULT 357
ID AAK77913 standard; DNA; 644 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32725.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 644;
Best Local Similarity 83.7%; Pred. No. 5.4e-48;
RESULT 358
ID AAK77915 standard; DNA; 646 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32727.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 646;
Best Local Similarity 83.7%; Pred. No. 5.4e-48;
RESULT 359
ID AAI84724 standard; cDNA; 777 BP.
DE Human polynucleotide SEQ ID NO 4784.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.4%; Score 203.4; DB 4; Length 777;
Best Local Similarity 79.7%; Pred. No. 5.8e-48;
RESULT 360
ID ACN39520 standard; cDNA; 2068 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325729, SEQ ID NO:3715.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GENTH) GENTECH INC.
Query Match 22.4%; Score 203.4; DB 13; Length 2068;
Best Local Similarity 81.3%; Pred. No. 8.5e-48;
RESULT 361
ID AAK77914 standard; DNA; 2558 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32726.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 2558;
Best Local Similarity 83.7%; Pred. No. 9.2e-48;
RESULT 362
ID AAL04534 standard; DNA; 4067 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7222.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 363
ID AAL04537 standard; DNA; 4067 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7225.
PN WO200155320-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 364
ID ABL97457 standard; DNA; 4067 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2109.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 365
ID ABL97460 standard; DNA; 4067 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2112.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 366
ID AAK77916 standard; DNA; 7759 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32728.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 7759;
Best Local Similarity 83.7%; Pred. No. 1.4e-47;
RESULT 367
ID AAK73223 standard; DNA; 31051 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28035.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 31051;
Best Local Similarity 77.9%; Pred. No. 2.4e-47;
RESULT 368
ID AAK89112 standard; DNA; 32190 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2688.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 369
ID AAS31862 standard; DNA; 32190 BP.
DE Human liver associated genomic DNA #36.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 5; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 370
ID AAB90217 standard; DNA; 32190 BP.
DE Human liver antigen HPLS161 genomic sequence, SEQ ID NO:338.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.4%; Score 203.4; DB 6; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 371
ID ADL15130 standard; DNA; 32190 BP.
DE Human liver-related genomic DNA - SEQ ID 338.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 11; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 372
ID AAB69695 standard; DNA; 56737 BP.
DE Human hypoxanthine-guanine phosphoribosyltransferase (HPRRT) gene.
PN US2002102731-A1.

PD 01-AUG-2002.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 22.4%; Score 203.4; DB 6; Length 56737;
Best Local Similarity 83.8%; Pred. No. 3e-47;
RESULT 373
ID ADL08126 standard; DNA; 191395 BP.
DE Human gene associated with low HDL-C PA12.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 22.4%; Score 203.4; DB 12; Length 191395;
Best Local Similarity 83.8%; Pred. No. 4.9e-47;
RESULT 374
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.4%; Score 203.4; DB 13; Length 238417;
Best Local Similarity 83.8%; Pred. No. 5.3e-47;
RESULT 375
ID ABEV74806 standard; cDNA; 2009 BP.
DE Signalase 11.22 coding sequence.
PN CN1345931-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.
Query Match 22.4%; Score 203.2; DB 6; Length 2009;
Best Local Similarity 83.0%; Pred. No. 9.6e-48;
RESULT 376
ID AAF97867 standard; DNA; 13161 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:81.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 22.4%; Score 203.2; DB 5; Length 13161;
Best Local Similarity 83.3%; Pred. No. 2e-47;
RESULT 377
ID AAK78275 standard; DNA; 35959 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.2; DB 4; Length 35959;
Best Local Similarity 78.7%; Pred. No. 2.9e-47;
RESULT 378
ID ADL13850 standard; DNA; 180550 BP.
DE Osteoarthritis-associated polymorphic nucleotide #382.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.4%; Score 203.2; DB 10; Length 180550;
Best Local Similarity 81.8%; Pred. No. 5.4e-47;
RESULT 379
ID ACN44398 standard; DNA; 194883 BP.
DE Human genomic sequence hCG20056.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.4%; Score 203.2; DB 11; Length 194883;
Best Local Similarity 75.1%; Pred. No. 5.6e-47;
RESULT 380
ID ABD33276 standard; DNA; 256190 BP.
DE Human cancer-associated (CA) gene HD07-048.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.4%; Score 203.2; DB 13; Length 256190;
Best Local Similarity 83.3%; Pred. No. 6.2e-47;
RESULT 381
ID AAK80969 standard; DNA; 6187 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35781.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203; DB 4; Length 6187;
Best Local Similarity 81.7%; Pred. No. 1.7e-47;
RESULT 382
ID ABRN9931 standard; DNA; 99014 BP.
DE Gene #1429 used to diagnose liver cancer.
PN WO200228103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.4%; Score 203; DB 6; Length 99014;
Best Local Similarity 76.4%; Pred. No. 4.9e-47;
RESULT 383
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbm168.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Query Match 22.4%; Score 203; DB 4; Length 114793;
Best Local Similarity 84.1%; Pred. No. 5.2e-47;
RESULT 384
ID ACN44170 standard; DNA; 196686 BP.
DE Human genomic sequence hCG39530.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.4%; Score 203; DB 11; Length 196686;
Best Local Similarity 83.7%; Pred. No. 6.4e-47;
RESULT 385
ID ADQ97523 standard; DNA; 215974 BP.
DE Human cancer associated sequence HD09-008, SEQ ID 500.
PN WO2004060304-A2.
PD 22-UTL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.4%; Score 203; DB 12; Length 215974;
Best Local Similarity 81.7%; Pred. No. 6.6e-47;
RESULT 386
ID AAD04910 standard; cDNA; 2013 BP.
DE Human secreted protein-encoding gene 4 cDNA clone HSLH186, SEQ ID NO:23.
PN WO200134799-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 2013;
Best Local Similarity 74.0%; Pred. No. 1.3e-47;
RESULT 387
ID AAL04936 standard; DNA; 3753 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7624.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 3753;
Best Local Similarity 79.2%; Pred. No. 1.6e-47;
RESULT 388
ID ABL97830 standard; DNA; 3753 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2482.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 3753;
Best Local Similarity 79.2%; Pred. No. 1.6e-47;
RESULT 389
ID AAD04901 standard; cDNA; 3781 BP.
DE Human secreted protein-encoding gene 4 cDNA clone HSLH186, SEQ ID NO:14.
PN WO200134799-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 3781;
Best Local Similarity 74.0%; Pred. No. 1.6e-47;
RESULT 390
ID AAK71815 standard; DNA; 14448 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26627.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 391
ID AAK87580 standard; DNA; 14448 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42392.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 392
ID AAK73111 standard; DNA; 14448 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27923.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 393
ID AAI62922 standard; DNA; 14448 BP.
DE Human genomic DNA SEQ ID NO 250.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 394
ID AAK73116 standard; DNA; 14451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27928.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 395
ID AAK71818 standard; DNA; 14451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26630.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 396
ID AAK87587 standard; DNA; 14451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42399.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 397
ID AAI62925 standard; DNA; 14451 BP.
DE Human genomic DNA SEQ ID NO 253.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 398
ID AAL03917 standard; DNA; 22299 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6605.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 22299;
Best Local Similarity 83.6%; Pred. No. 3.2e-47;
RESULT 399
ID AAS40317 standard; DNA; 22299 BP.
DE DNA encoding human prostate cancer antigen, Seq ID No 469.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.4%; Score 202.8; DB 5; Length 22299;
 Best Local Similarity 83.6%; Pred. No. 3.2e-47;
 RESULT 400
 ID ADJ09523 standard; DNA; 22299 BP.
 DE Human prostate cancer associated gene-related DNA SeqID469.
 PN US2003054373-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.4%; Score 202.8; DB 11; Length 22299;
 Best Local Similarity 83.6%; Pred. No. 3.2e-47;
 RESULT 401
 ID ADM97421 standard; DNA; 26865 BP.
 DE Prostate and breast cancer associated human gene CYP17.
 PN WO2004028346-A2.
 PD 08-APR-2004.
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 Query Match 22.4%; Score 202.8; DB 12; Length 26865;
 Best Local Similarity 78.9%; Pred. No. 3.4e-47;
 RESULT 402
 ID AAD50021 standard; DNA; 27067 BP.
 DE Human secreted protein encoding gene.
 Query Match 22.4%; Score 202.8; DB 10; Length 27067;
 Best Local Similarity 83.6%; Pred. No. 3.4e-47;
 RESULT 403
 ID AAA35003 standard; DNA; 56583 BP.
 DE Human adenocarcinoma receptor related polynucleotide SEQ ID NO:2692.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.4%; Score 202.8; DB 3; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 404
 ID AAF21125 standard; DNA; 56583 BP.
 DE Human low adenocarcinoma antileukemia oligonucleotide related sequence #2692.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.4%; Score 202.8; DB 3; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 405
 ID AB296819 standard; DNA; 56583 BP.
 DE Human nucleic acid sequence.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIDEMISIS PHARM INC.
 Query Match 22.4%; Score 202.8; DB 10; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 406
 ID ABD20668 standard; DNA; 56583 BP.
 DE Human pulmonary and inflammatory target DNA #279.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIDEMISIS PHARM INC.
 Query Match 22.4%; Score 202.8; DB 11; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 407
 ID ACN44066 standard; DNA; 99886 BP.
 DE Human genomic sequence hCG15674.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.4%; Score 202.8; DB 11; Length 99886;
 Best Local Similarity 79.2%; Pred. No. 5.6e-47;
 RESULT 408
 ID ADQ17329 standard; DNA; 101685 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 22.4%; Score 202.8; DB 12; Length 101685;
 Best Local Similarity 79.2%; Pred. No. 5.7e-47;
 RESULT 409

ID ACN45054 standard; DNA; 133632 BP.
 DE Human genomic sequence hCG28560.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.4%; Score 202.8; DB 11; Length 133632;
 Best Local Similarity 76.0%; Pred. No. 6.3e-47;
 RESULT 410
 ID ADC56769 standard; DNA; 1051 BP.
 DE DNA (SeqID 4) related to the human thymidylate acid synthetase gene.
 PN JP2003102480-A.
 PD 08-APR-2003.
 PA (SRLS-) SRL KK.
 Query Match 22.3%; Score 202.6; DB 10; Length 1051;
 Best Local Similarity 81.7%; Pred. No. 1.1e-47;
 RESULT 411
 ID AAS34702 standard; DNA; 3147 BP.
 DE Human DNA for a novel foetal antigen, SEQ ID NO 2126.
 PN WO200155312-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202.6; DB 5; Length 3147;
 Best Local Similarity 83.1%; Pred. No. 1.7e-47;
 RESULT 412
 ID AAF5338 standard; cDNA; 3200 BP.
 DE Human TGF-beta receptor cDNA clone HDXK45.
 PN WO200112670-A1.
 PD 22-FEB-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202.6; DB 4; Length 3200;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 413
 ID ABR14000 standard; cDNA; 3353 BP.
 DE cDNA encoding human protein kinase 3700.
 PN WO200224921-A2.
 PD 28-MAR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 22.3%; Score 202.6; DB 6; Length 3353;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 414
 ID ADL14160 standard; cDNA; 3353 BP.
 DE Novel human gene 3700 cDNA.
 PN US2004058355-A1.
 PD 25-MAR-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 22.3%; Score 202.6; DB 12; Length 3353;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 415
 ID AAD26459 standard; cDNA; 3360 BP.
 DE Human kinase PKIN-12 cDNA.
 PN WO200196547-A2.
 PD 20-DEC-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.3%; Score 202.6; DB 6; Length 3360;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 416
 ID AAK94280 standard; cDNA; 3395 BP.
 DE Human full-length cDNA, SEQ ID NO: 2918.
 PN BP130094-A2.
 PD 05-SEP-2001.
 PA (HELT-) HELIX RES INST.
 Query Match 22.3%; Score 202.6; DB 4; Length 3395;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 417
 ID ADJ30885 standard; cDNA; 3395 BP.
 DE Full length human cDNA clone SeqID 2918.
 PN BP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 22.3%; Score 202.6; DB 12; Length 3395;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 418
 ID ABX71420 standard; cDNA; 3443 BP.

DE Human cell cycle-associated cDNA from clone DKFzphc03_7j3.
PN WO200112659-A2.
PD 22-FEB-2001.
ID (GENH-) GERMAN HUMAN GENOME PROJECT.
Query Match 22.3%; Score 202.6; DB 5; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 419
ID ADF76964 standard; cDNA; 3443 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 639.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GEMENTECH INC.
Query Match 22.3%; Score 202.6; DB 10; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 420
ID ADF81952 standard; DNA; 3443 BP.
DE Leukemia-related DNA sequence #2508.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFB/) HAFERLACH T.
PA (SCHC/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 22.3%; Score 202.6; DB 10; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 421
ID ADO20171 standard; cDNA; 3443 BP.
DE Human PRO polynucleotide #540.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GEMENTECH INC.
Query Match 22.3%; Score 202.6; DB 12; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 422
ID AAK66979 standard; DNA; 4646 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23791.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 4646;
Best Local Similarity 82.3%; Pred. No. 2e-47;
RESULT 423
ID ABA20357 standard; DNA; 11585 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12688.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 5; Length 11585;
Best Local Similarity 83.3%; Pred. No. 2.8e-47;
RESULT 424
ID AAS36927 standard; DNA; 20869 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2427.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 425
ID AAK85001 standard; DNA; 20869 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39813.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 426
ID ABA16245 standard; DNA; 20869 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8576.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 5; Length 20869;

Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 427
ID ADB47621 standard; DNA; 20869 BP.
DE Human cardiovascular system related genomic DNA #1187.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 10; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 428
ID ADJ09039 standard; DNA; 20869 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2427.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 13; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 429
ID AAK82338 standard; DNA; 48908 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 48908;
Best Local Similarity 81.7%; Pred. No. 4.9e-47;
RESULT 430
ID AAK66125 standard; DNA; 556 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20937.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 556;
Best Local Similarity 82.6%; Pred. No. 1e-47;
RESULT 431
ID AAK66126 standard; DNA; 556 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20938.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 556;
Best Local Similarity 82.6%; Pred. No. 1e-47;
RESULT 432
ID AAS36105 standard; DNA; 32195 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1605.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 433
ID AAS31538 standard; DNA; 32195 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 617.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 434
ID AAS31532 standard; DNA; 32195 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 611.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 435
ID ABA44045 standard; DNA; 32195 BP.
DE Genomic DNA encoding novel central nervous system protein #260.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;

RESULT 436
ID ABO6686 standard; DNA; 32195 BP.
DE Human polynucleotide SEQ ID NO 611.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.3%; Score 202.4; DB 6; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 437
ID ABO66862 standard; DNA; 32195 BP.
DE Human polynucleotide SEQ ID NO 617.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.3%; Score 202.4; DB 6; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 438
ID ADC11143 standard; DNA; 32195 BP.
DE Human DNA from extracellular matrix gene 112 #1.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 10; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 439
ID ADC11149 standard; DNA; 32195 BP.
DE Human DNA from extracellular matrix gene 113 #1.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 10; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 440
ID ADE46799 standard; DNA; 32195 BP.
DE Human cardiovascular system related genomic DNA #365.
PN US2003059808-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 10; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 441
ID ADI55030 standard; DNA; 32195 BP.
DE Novel human protein genomic DNA seq id 1233.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.3%; Score 202.4; DB 13; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 442
ID ADJ08217 standard; DNA; 32195 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1605.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 13; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 443
ID ACN37205 standard; DNA; 34079 BP.
DE Human periodontal disease related gene COL18A1 SEQ ID NO.115.
Query Match 22.3%; Score 202.4; DB 13; Length 34079;
Best Local Similarity 81.2%; Pred. No. 4.9e-47;
RESULT 444
ID AAK83781 standard; DNA; 37664 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO.38593.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.3%; Score 202.4; DB 4; Length 37664;
Best Local Similarity 81.2%; Pred. No. 5e-47;
RESULT 445
ID ADJ18757 standard; DNA; 43712 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1576.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.3%; Score 202.4; DB 12; Length 43712;
Best Local Similarity 77.6%; Pred. No. 5.3e-47;
RESULT 446
ID AAK83782 standard; DNA; 61710 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO.38594.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.2; DB 4; Length 61710;
Best Local Similarity 81.2%; Pred. No. 6.1e-47;
RESULT 447
ID AAL57580 standard; cDNA; 93273 BP.
DE Human GTPase activating protein-like cDNA.
PN WO2003059148-A2.
PD 24-JUL-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 22.3%; Score 202.4; DB 9; Length 93273;
Best Local Similarity 79.9%; Pred. No. 7.2e-47;
RESULT 448
ID ABD32827 standard; DNA; 129381 BP.
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.3%; Score 202.4; DB 13; Length 129381;
Best Local Similarity 81.2%; Pred. No. 8.1e-47;
RESULT 449
ID AAZ50359 standard; DNA; 9365 BP.
DE Human CD39-L4 genomic DNA.
PN WO200004041-A2.
PD 27-JAN-2000.
PA (HYSE-) HYSEQ INC.
Query Match 22.3%; Score 202.2; DB 3; Length 9365;
Best Local Similarity 78.6%; Pred. No. 3.4e-47;
RESULT 450
ID AAF63405 standard; DNA; 9365 BP.
DE Human CD39 like protein CD39-L4 partial DNA sequence.
PN WO200110205-A1.
PD 15-FEB-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.3%; Score 202.2; DB 4; Length 9365;
Best Local Similarity 78.6%; Pred. No. 3.4e-47;
RESULT 451
ID AAF63406 standard; DNA; 14747 BP.
DE Human CD39 like protein CD39-L4 genomic DNA sequence.
PN WO200110205-A1.
PD 15-FEB-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.3%; Score 202.2; DB 4; Length 14747;
Best Local Similarity 78.6%; Pred. No. 4e-47;
RESULT 452
ID AAF63407 standard; DNA; 15977 BP.
DE Human CD39 like protein CD39-L4 genomic DNA sequence #2.
PN WO200110205-A1.
PD 15-FEB-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.3%; Score 202.2; DB 4; Length 15977;
Best Local Similarity 78.6%; Pred. No. 4.1e-47;
RESULT 453
ID ACN44382 standard; DNA; 30558 BP.
DE Human genomic sequence hCG15773.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.3%; Score 202.2; DB 11; Length 30558;
Best Local Similarity 85.8%; Pred. No. 5.3e-47;
ID ABRN96931 standard; DNA; 99014 BP.
DE Gene #3429 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.3%; Score 202.2; DB 6; Length 99014;
Best Local Similarity 79.5%; Pred. No. 8.4e-47;
RESULT 455
ID ACN43994 standard; DNA; 109586 BP.
DE Human genomic sequence hCG23847.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGE-) SAGES DISCOVERY
Query Match 22.3%; Score 202.2; DB 11; Length 109586;
Best Local Similarity 83.2%; Pred. No. 8.7e-47;
RESULT 456
ID ADP03055 standard; cDNA; 124987 BP.
DE Human housekeeping gene cDNA #96.
PN JP200413552-A.
PD 13-MAY-2004.
PA (NIG) NGK INSULATORS LTD.
Query Match 22.3%; Score 202.2; DB 12; Length 124987;
Best Local Similarity 82.1%; Pred. No. 9.1e-47;
RESULT 457
ID ADS88553 standard; cDNA; 124990 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:96.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIG) NGK INSULATORS LTD.
Query Match 22.3%; Score 202.2; DB 13; Length 124990;
Best Local Similarity 82.1%; Pred. No. 9.1e-47;
RESULT 458
ID ACH25975 standard; cDNA; 502 BP.
DE Human adult ovary cDNA #3355.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 22.3%; Score 202; DB 9; Length 502;
Best Local Similarity 72.7%; Pred. No. 1.2e-47;
RESULT 459
ID ADD19251 standard; cDNA; 843 BP.
DE Human cDNA from secreted protein gene 68.
PN WO2003052377-A2.
PD 26-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 843;
Best Local Similarity 81.5%; Pred. No. 1.5e-47;
RESULT 460
ID ADD19217 standard; cDNA; 878 BP.
DE Human cDNA from secreted protein gene 34.
PN WO2003052377-A2.
PD 26-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 878;
Best Local Similarity 81.5%; Pred. No. 1.5e-47;
RESULT 461
ID ADM02980 standard; cDNA; 1960 BP.
DE Human cDNA of the invention SEQ ID NO:1665.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.3%; Score 202; DB 11; Length 1960;
Best Local Similarity 78.2%; Pred. No. 2.1e-47;
RESULT 462
ID ADD18777 standard; DNA; 8672 BP.
DE Human disease related protein DNA sequence SeqID208.

PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 22.3%; Score 202; DB 10; Length 8672;
Best Local Similarity 74.6%; Pred. No. 3.7e-47;
RESULT 463
ID AAK72319 standard; DNA; 15090 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27131.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 4; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 464
ID ABR69842 standard; DNA; 15090 BP.
DE Human secreted protein gene 22 genomic DNA fragment #3.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 6; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 465
ID ABR69843 standard; DNA; 15090 BP.
DE Human secreted protein gene 22 genomic DNA fragment #4.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 6; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 466
ID ACC50857 standard; cDNA; 15090 BP.
DE Human secreted protein BAC clone SEQ ID NO 1037.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 467
ID ACC50858 standard; cDNA; 15090 BP.
DE Human secreted protein BAC clone SEQ ID NO 1038.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 468
ID ABR71480 standard; DNA; 15090 BP.
DE Secreted protein gene 12 genomic fragment HAUAI83, SEQ ID NO:590.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 469
ID ABR71479 standard; DNA; 15090 BP.
DE Secreted protein gene 12 genomic fragment HAUAI83, SEQ ID NO:589.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 470
ID ADB91835 standard; DNA; 15090 BP.
DE Human secreted protein related DNA #SEQ ID 781.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 9; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 471
ID ADB91836 standard; DNA; 15090 BP.
DE Human secreted protein related DNA #SEQ ID 782.
PN WO2003004622-A2.

PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 9; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 472
ID ADCT74610 standard; DNA; 15090 BP.
DE Human secreted protein-related DNA - SEQ ID 1243.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 473
ID ADCT74611 standard; DNA; 15090 BP.
DE Human secreted protein-related DNA - SEQ ID 1244.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 474
ID ADD38131 standard; cDNA; 15090 BP.
DE cDNA clone in ATCC deposit #25.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 475
ID ADD38130 standard; cDNA; 15090 BP.
DE cDNA clone in ATCC deposit #24.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 476
ID ADA57724 standard; DNA; 15090 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 477
ID ADA57725 standard; DNA; 15090 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 478
ID ADA02630 standard; DNA; 32433 BP.
DE Human FLT3 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.3%; Score 202; DB 9; Length 32433;
Best Local Similarity 80.3%; Pred. No. 6.2e-47;
RESULT 480
ID ADB95878 standard; DNA; 32433 BP.
DE Human FLT3 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.3%; Score 202; DB 10; Length 32433;
Best Local Similarity 80.3%; Pred. No. 6.2e-47;
RESULT 481
ID ABD33115 standard; DNA; 69652 BP.
DE Human cancer-associated (CA) gene HD07-011.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.3%; Score 202; DB 13; Length 69652;
Best Local Similarity 77.1%; Pred. No. 8.3e-47;
RESULT 482
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.3%; Score 202; DB 13; Length 238417;
Best Local Similarity 82.8%; Pred. No. 1.3e-46;
RESULT 483
ID AAK79410 standard; DNA; 4883 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34222.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 4883;
Best Local Similarity 78.1%; Pred. No. 3.4e-47;
RESULT 484
ID ADQ64434 standard; cDNA; 8331 BP.
DE Novel human cDNA sequence #1595.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.2%; Score 201.8; DB 12; Length 8331;
Best Local Similarity 83.5%; Pred. No. 4.2e-47;
RESULT 485
ID AAS33461 standard; DNA; 9192 BP.
DE DNA encoding human secreted protein, Seq ID No 744.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 9192;
Best Local Similarity 81.0%; Pred. No. 4.4e-47;
RESULT 486
ID AAL36577 standard; DNA; 11991 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2942.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 487
ID AAL07205 standard; DNA; 11991 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9893.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 488
ID AAX59565 standard; cDNA; 11991 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1909.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BAR/) BARASH S C.
Query Match 22.2%; Score 201.8; DB 8; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 489
ID ADJ30315 standard; DNA; 11991 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2942.
PN US2004009488-A1.

PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 12; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 490
ID AAS33462 standard; DNA; 25715 BP.
DE DNA encoding human secreted protein, Seq ID No 745.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 25715;
Best Local Similarity 81.0%; Pred. No. 6.5e-47;
RESULT 491
ID ACN44690 standard; DNA; 47243 BP.
DE Human genomic sequence hCG15501.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.8; DB 11; Length 47243;
Best Local Similarity 82.3%; Pred. No. 8.2e-47;
RESULT 492
ID ADM97422 standard; DNA; 76341 BP.
DE Prostate and breast cancer associated human gene SMD5A2.
PN WO2004028346-A2.
PD 08-APR-2004.
PA (AMGH-) AMERSHAM BIOSCIENCES SV CORP.
Query Match 22.2%; Score 201.8; DB 12; Length 76341;
Best Local Similarity 83.5%; Pred. No. 9.9e-47;
RESULT 493
ID ADQ9518 standard; DNA; 100762 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:154.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.8; DB 13; Length 100762;
Best Local Similarity 78.8%; Pred. No. 1.1e-46;
RESULT 494
Query Match 22.2%; Score 201.8; DB 10; Length 110000;
Best Local Similarity 78.6%; Pred. No. 1.1e-46;
RESULT 495
ID AAD2697 standard; DNA; 160552 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (RESC-) UNIV CALIFORNIA.
Query Match 22.2%; Score 201.8; DB 4; Length 160552;
Best Local Similarity 81.0%; Pred. No. 1.3e-46;
RESULT 496
ID ABD33232 standard; DNA; 161531 BP.
DE Human cancer-associated (CA) gene HD07-038.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.8; DB 13; Length 161531;
Best Local Similarity 81.0%; Pred. No. 1.3e-46;
RESULT 497
ID ADI33775 standard; DNA; 173805 BP.
DE Osteoarthritis-associated polymorphic nucleotide #307.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201.8; DB 10; Length 173805;
Best Local Similarity 83.5%; Pred. No. 1.4e-46;
RESULT 498
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.8; DB 11; Length 175077;
Best Local Similarity 79.9%; Pred. No. 1.4e-46;
RESULT 499
ID ADE43315 standard; DNA; 202100 BP.

DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003
PA (NEUR-) NEUROGENETICS INC.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 22.2%; Score 201.8; DB 10; Length 202100;
Best Local Similarity 81.2%; Pred. No. 1.4e-46;
RESULT 500
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 22.2%; Score 201.8; DB 12; Length 202100;
Best Local Similarity 81.2%; Pred. No. 1.4e-46;
RESULT 501
ID ADP75168 standard; DNA; 276820 BP.
DE Human ADAMTS2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 22.2%; Score 201.8; DB 11; Length 276820;
Best Local Similarity 83.7%; Pred. No. 1.6e-46;
RESULT 502
ID AAS32713 standard; DNA; 2666 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 667.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 2666;
Best Local Similarity 77.7%; Pred. No. 3.1e-47;
RESULT 503
ID ADRO6632 standard; cDNA; 3677 BP.
DE Full length human cDNA useful for treating neurological disease Seq 128.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.2%; Score 201.6; DB 13; Length 3677;
Best Local Similarity 83.0%; Pred. No. 3.5e-47;
RESULT 504
ID AAK91537 standard; DNA; 8896 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5113.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 505
ID AAI57794 standard; DNA; 8896 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 331.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 506
ID AAS32712 standard; DNA; 8896 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 666.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 507
ID ABS99971 standard; DNA; 8896 BP.
DE Genomic DNA #175 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.2%; Score 201.6; DB 6; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;

RESULT 508
 ID ADB9124 standard; DNA; 8896 BP.
 DE Human colorectal cancer related polypeptide DNA #175.
 PN US2003054420-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 10; Length 8896;
 Best Local Similarity 77.7%; Pred. No. 4.9e-47;
 RESULT 509
 ID AAL60675 standard; DNA; 12430 BP.
 DE Human ataxia telangiectasia and Rad-3-related (ATR) clone8 gene.
 PN WO2003044214-A2.
 PD 30-MAY-2003.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 Query Match 22.2%; Score 201.6; DB 9; Length 12430;
 Best Local Similarity 85.5%; Pred. No. 5.6e-47;
 RESULT 510
 ID AAL60676 standard; DNA; 14405 BP.
 DE PDC353 knockout construct DNA.
 PN WO2003044214-A2.
 PD 30-MAY-2003.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 Query Match 22.2%; Score 201.6; DB 9; Length 14405;
 Best Local Similarity 85.5%; Pred. No. 5.9e-47;
 RESULT 511
 ID AAK84138 standard; DNA; 17758 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 17758;
 Best Local Similarity 83.0%; Pred. No. 6.4e-47;
 RESULT 512
 ID AAI99172 standard; DNA; 32134 BP.
 DE Human excretory related polynucleotide SEQ ID NO 936.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 32134;
 Best Local Similarity 77.7%; Pred. No. 8.1e-47;
 RESULT 513
 ID AAI65522 standard; DNA; 32134 BP.
 DE Human kidney related polynucleotide SEQ ID NO 837.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 5; Length 32134;
 Best Local Similarity 77.7%; Pred. No. 8.1e-47;
 RESULT 514
 ID AAI99173 standard; DNA; 32192 BP.
 DE Human excretory related polynucleotide SEQ ID NO 937.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 32192;
 Best Local Similarity 77.7%; Pred. No. 8.1e-47;
 RESULT 515
 ID AAI63523 standard; DNA; 32192 BP.
 DE Human kidney related polynucleotide SEQ ID NO 838.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 5; Length 32192;
 Best Local Similarity 77.7%; Pred. No. 8.1e-47;
 RESULT 516
 ID AAK69767 standard; DNA; 35100 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24579.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 35100;
 Best Local Similarity 77.7%; Pred. No. 8.3e-47;
 RESULT 517

ID AAK65700 standard; DNA; 35100 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20512.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 35100;
 Best Local Similarity 77.7%; Pred. No. 8.3e-47;
 RESULT 518
 ID AAK69766 standard; DNA; 35115 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24578.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 35115;
 Best Local Similarity 77.7%; Pred. No. 8.3e-47;
 RESULT 519
 ID AAK65699 standard; DNA; 35115 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20511.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.2%; Score 201.6; DB 4; Length 35115;
 Best Local Similarity 77.7%; Pred. No. 8.3e-47;
 RESULT 520
 ID ACN44146 standard; DNA; 50602 BP.
 DE Human genomic sequence HCG28572.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.2%; Score 201.6; DB 11; Length 50602;
 Best Local Similarity 81.5%; Pred. No. 9.6e-47;
 RESULT 521
 ID AAX90201 standard; DNA; 119950 BP.
 DE Human yeast gene.
 PN WO9935290-A1.
 PD 15-JUL-1999.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 22.2%; Score 201.6; DB 2; Length 119950;
 Best Local Similarity 81.7%; Pred. No. 1.3e-46;
 RESULT 522
 ID ADP65423 standard; DNA; 154068 BP.
 DE Human sequence from clone RP11-363122 on chromosome 1, complete DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 22.2%; Score 201.6; DB 11; Length 154068;
 Best Local Similarity 81.2%; Pred. No. 1.5e-46;
 RESULT 523
 ID ACH21579 standard; cDNA; 406 BP.
 DE Human adult liver cDNA #1191.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABART I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 22.2%; Score 201.4; DB 9; Length 406;
 Best Local Similarity 82.4%; Pred. No. 1.7e-47;
 RESULT 524
 ID AAH18654 standard; cDNA; 6020 BP.
 DE Human cDNA sequence SEQ ID NO:18897.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 22.2%; Score 201.4; DB 4; Length 6020;
 Best Local Similarity 72.9%; Pred. No. 4.8e-47;
 RESULT 525
 ID AAV34455 standard; DNA; 11722 BP.
 DE Human MHC class I chain-related gene A (MICA).
 PN WO9819167-A2.
 PD 07-MAY-1998.
 PA (HOTC-) HUTCHINSON CANCER RES CENT FRED.

Query Match 22.2%; Score 201.4; DB 2; Length 11722;
Best Local Similarity 83.6%; Pred. No. 6.2e-47;
RESULT 526
ID ADE06443 standard; cDNA; 11722 BP.
DE Human MICA cDNA SEQ ID NO:1.
PN WO2003089616-A2.
PD 30-OCT-2003.
PA (HUTC-) HUTCHINSON CANCER RES CENT FRID.
Query Match 22.2%; Score 201.4; DB 10; Length 11722;
Best Local Similarity 83.6%; Pred. No. 6.2e-47;
RESULT 527
ID AAK0159 standard; DNA; 15783 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3735.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.4; DB 4; Length 15783;
Best Local Similarity 81.2%; Pred. No. 7e-47;
RESULT 528
ID AAS39803 standard; DNA; 15783 BP.
DE Genomic sequence #222 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.4; DB 5; Length 15783;
Best Local Similarity 81.2%; Pred. No. 7e-47;
RESULT 529
ID ADB32763 standard; DNA; 15783 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 700.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BAR/) BARASH S C.
Query Match 22.2%; Score 201.4; DB 9; Length 15783;
Best Local Similarity 81.2%; Pred. No. 7e-47;
RESULT 530
ID ABA18491 standard; DNA; 16159 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10822.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.4; DB 5; Length 16159;
Best Local Similarity 85.0%; Pred. No. 7.1e-47;
RESULT 531
ID ACN44470 standard; DNA; 42954 BP.
DE Human genomic sequence hCG40844.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.4; DB 11; Length 42954;
Best Local Similarity 81.2%; Pred. No. 1e-46;
RESULT 532
ID ADC60735 standard; DNA; 50000 BP.
DE Human elingshot-related DNA 9.
PN JP2003102483-A.
PD 08-APR-2003.
PA (KAG-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 22.2%; Score 201.4; DB 10; Length 50000;
Best Local Similarity 82.4%; Pred. No. 1.1e-46;
RESULT 533
ID ACN44290 standard; DNA; 59856 BP.
DE Human genomic sequence hCG24994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.4; DB 11; Length 59856;
Best Local Similarity 81.2%; Pred. No. 1.2e-46;
RESULT 534
ID AAD50739 standard; DNA; 64467 BP.
DE Human Kinase gene.
Query Match 22.2%; Score 201.4; DB 8; Length 64467;
Best Local Similarity 74.6%; Pred. No. 1.2e-46;

RESULT 535
ID ACH00100 standard; DNA; 64467 BP.
DE Human kinase protein genomic DNA.
Query Match 22.2%; Score 201.4; DB 9; Length 64467;
Best Local Similarity 74.6%; Pred. No. 1.2e-46;
RESULT 536
ID ADD15783 standard; DNA; 64467 BP.
DE Human MEK kinase subfamily kinase genomic DNA.
PN US6582946-B1.
PD 24-JUN-2003.
PA (APPL-) APPLERA CORP.
Query Match 22.2%; Score 201.4; DB 10; Length 64467;
Best Local Similarity 74.6%; Pred. No. 1.2e-46;
RESULT 537
ID ABL64403 standard; DNA; 167343 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2740.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.2%; Score 201.4; DB 6; Length 167343;
Best Local Similarity 76.1%; Pred. No. 1.7e-46;
RESULT 538
ID ABL67239 standard; DNA; 167343 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5576.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.2%; Score 201.4; DB 6; Length 167343;
Best Local Similarity 76.1%; Pred. No. 1.7e-46;
RESULT 539
ID ABD32715 standard; DNA; 337344 BP.
DE Human cancer-associated genomic DNA HD14-044.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.4; DB 13; Length 337344;
Best Local Similarity 81.2%; Pred. No. 2.3e-46;
RESULT 540
ID AAH14294 standard; cDNA; 1557 BP.
DE Human cDNA sequence SEQ ID NO:11638.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.2%; Score 201.2; DB 4; Length 1557;
Best Local Similarity 85.8%; Pred. No. 3.3e-47;
RESULT 541
ID ADQ19190 standard; DNA; 1557 BP.
DE Human boft clesue sarcoma-upregulated DNA - SEQ ID 2009.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.2%; Score 201.2; DB 12; Length 1557;
Best Local Similarity 85.8%; Pred. No. 3.3e-47;
RESULT 542
ID AAK87586 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42398.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 543
ID AAK71817 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26629.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 544
ID AAK73115 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27927.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 545
ID AAI62924 standard; DNA; 14426 BP.
DE Human genomic DNA SEQ ID NO 252.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 546
ID ABZ74676 standard; DNA; 14426 BP.
DE Secreted protein gene 391 genomic fragment HE8FC45, SEQ ID NO:1823.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 8; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 547
ID ABZ68198 standard; DNA; 14426 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1721.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 10; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 548
ID ABA19324 standard; DNA; 27733 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11655.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 5; Length 27733;
Best Local Similarity 79.6%; Pred. No. 9.9e-47;
RESULT 549
ID AAK66517 standard; DNA; 27869 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:21329.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 27869;
Best Local Similarity 76.6%; Pred. No. 9.9e-47;
RESULT 550
ID ABA19635 standard; DNA; 27869 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11966.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 5; Length 27869;
Best Local Similarity 76.6%; Pred. No. 9.9e-47;
RESULT 551
ID ADQ97164 standard; DNA; 145985 BP.
DE Human cancer associated sequence HD1-08-009, SEQ ID 140.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.2; DB 12; Length 145985;
Best Local Similarity 83.1%; Pred. No. 1.9e-46;
RESULT 552
ID ABD33272 standard; DNA; 227246 BP.
DE Human cancer-associated (CA) gene HD07-047.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.2; DB 13; Length 227246;
Best Local Similarity 80.7%; Pred. No. 2.2e-46;
RESULT 553
ID AAK65169 standard; DNA; 370 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:19981.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 4; Length 370;
Best Local Similarity 81.4%; Pred. No. 2.2e-47;
RESULT 554
ID ABV46137 standard; cDNA; 477 BP.
DE Human prostate expression marker cDNA 46128.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNium PREDICTIVE MEDICINE INC.
Query Match 22.2%; Score 201; DB 5; Length 477;
Best Local Similarity 81.4%; Pred. No. 2.4e-47;
RESULT 555
ID ABQ72599 standard; cDNA; 2616 BP.
DE Human MDR1 encoding cDNA SEQ ID NO 151.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201; DB 6; Length 2616;
Best Local Similarity 81.4%; Pred. No. 4.6e-47;
RESULT 556
ID ABD33085 standard; cDNA; 3404 BP.
DE Human cancer-associated (CA) cDNA HR07-004.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201; DB 13; Length 3404;
Best Local Similarity 81.4%; Pred. No. 5.1e-47;
RESULT 557
ID ADJ96554 standard; DNA; 3463 BP.
DE Human calcium/calmodulin-dependent protein kinase Nuak2 DNA SeqID 11.
PN WO2004006838-A2.
PD 22-JAN-2004.
PA (SUGR-) SUGEN INC.
Query Match 22.2%; Score 201; DB 12; Length 3463;
Best Local Similarity 81.4%; Pred. No. 5.1e-47;
RESULT 558
ID AAK74096 standard; DNA; 21777 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:28908.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 4; Length 21777;
Best Local Similarity 83.9%; Pred. No. 1e-46;
RESULT 559
ID ABA15939 standard; DNA; 24292 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8270.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 5; Length 24292;
Best Local Similarity 78.7%; Pred. No. 1.1e-46;
RESULT 560
ID AAK66336 standard; DNA; 25971 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:41148.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 4; Length 25971;
Best Local Similarity 73.7%; Pred. No. 1.1e-46;
RESULT 561
ID AAD44328 standard; DNA; 34667 BP.
DE Human transporter gene.
PN WO200248367-A2.
PD 20-JUN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 6; Length 34667;
Best Local Similarity 81.4%; Pred. No. 1.2e-46;
RESULT 562
ID ABD33084 standard; DNA; 39699 BP.
DE Human cancer-associated (CA) gene HD07-004.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201; DB 13; Length 39699;

Best Local Similarity 81.4%; Pred. No. 1.3e-46;
RESULT 563
ID ACN45050 standard; DNA; 41966 BP.
DE Human genomic sequence hCG39344.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201; DB 11; Length 41966;
Best Local Similarity 83.9%; Pred. No. 1.3e-46;
RESULT 564
ID ABL68262 standard; DNA; 62944 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6599.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALLON PHARM.
Query Match 22.2%; Score 201; DB 6; Length 62944;
Best Local Similarity 78.7%; Pred. No. 1.6e-46;
RESULT 565
ID ABL66947 standard; DNA; 62944 BP.
DE Lung cancer related gene sequence SEQ ID NO:5284.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALLON PHARM.
Query Match 22.2%; Score 201; DB 6; Length 62944;
Best Local Similarity 78.7%; Pred. No. 1.6e-46;
RESULT 566
ID ADL3941 standard; DNA; 125515 BP.
DE Osteoarthritis-associated polymorphic nucleotide #473.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201; DB 10; Length 125515;
Best Local Similarity 77.2%; Pred. No. 2e-46;
RESULT 567
ID ADC87620 standard; DNA; 144792 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2073.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 22.2%; Score 201; DB 10; Length 144792;
Best Local Similarity 84.5%; Pred. No. 2.1e-46;
RESULT 568
ID ADL3850 standard; DNA; 180550 BP.
DE Osteoarthritis-associated polymorphic nucleotide #382.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201; DB 10; Length 180550;
Best Local Similarity 81.4%; Pred. No. 2.3e-46;
RESULT 569
ID AB280229 standard; DNA; 249999 BP.
DE Human transdixin gene region genomic DNA SEQ ID NO:26.
PN WO2003016502-A2.
PD 27-FEB-2003.
PA (MCLA-) MCLAUGHLIN RES INST.
Query Match 22.2%; Score 201; DB 8; Length 249999;
Best Local Similarity 81.4%; Pred. No. 2.6e-46;
RESULT 570
ID ADC87619 standard; DNA; 349981 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2072.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 22.2%; Score 201; DB 10; Length 349981;
Best Local Similarity 84.5%; Pred. No. 3e-46;
RESULT 571
ID ACH29888 standard; cDNA; 390 BP.
DE Human testis cDNA #274.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.
DE (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 22.1%; Score 200.8; DB 9; Length 390;
Best Local Similarity 84.6%; Pred. No. 2.5e-47;
RESULT 572
ID ADB99093 standard; cDNA; 4421 BP.
DE Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #3.
PN US2003096750-A1.
PD 22-MAY-2003.
PA (TOMB/) TOMBRAN-TINK J.
PA (STEB/) STEBLE F R.
PA (CHAD/) CHADER G J.
PA (BECE/) BECERRA S P.
PA (JOHN/) JOHNSON L V.
PA (RODR/) RODRIGUEZ I R.
Query Match 22.1%; Score 200.8; DB 10; Length 4421;
Best Local Similarity 80.7%; Pred. No. 6.4e-47;
RESULT 573
ID ABS57269 standard; DNA; 4421 BP.
DE Partial sequence #3 of genomic DNA encoding human PEDF.
PN US6451763-B1.
PD 17-SEP-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.1%; Score 200.8; DB 10; Length 4421;
Best Local Similarity 80.7%; Pred. No. 6.4e-47;
RESULT 574
ID AAK9727 standard; DNA; 22645 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3303.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 575
ID AAL05495 standard; DNA; 22645 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8183.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 576
ID AAL04985 standard; DNA; 22645 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7673.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 577
ID ABL97878 standard; DNA; 22645 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2530.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 578
ID ABL98348 standard; DNA; 22645 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3000.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 579
ID AAK66931 standard; DNA; 30620 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21743.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.1%; Score 200.8; DB 4; Length 30620;
Best Local Similarity 80.9%; Pred. No. 1.3e-46;
RESULT 580
ID ADA02600 standard; DNA; 96593 BP.
DE Human RUNX1 carcinoma associated gene, SEQ ID NO:1118.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 9; Length 96593;
Best Local Similarity 85.8%; Pred. No. 2.1e-46;
RESULT 581
ID ADB72338 standard; DNA; 96593 BP.
DE Human RUNX1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 10; Length 96593;
Best Local Similarity 85.8%; Pred. No. 2.1e-46;
RESULT 582
ID ADB95848 standard; DNA; 96593 BP.
DE Human RUNX1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 10; Length 96593;
Best Local Similarity 85.8%; Pred. No. 2.1e-46;
RESULT 583
ID AAD1230 standard; DNA; 107820 BP.
DE Human ATP-binding cassette transporter ABC6 (MRP6) complementary gene.
Query Match 22.1%; Score 200.8; DB 4; Length 107820;
Best Local Similarity 84.9%; Pred. No. 2.2e-46;
RESULT 584
ID ACF62733 standard; DNA; 172984 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 8; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 585
ID ADB20848 standard; DNA; 172984 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 8; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 586
ID ADB87937 standard; DNA; 172984 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:661.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 10; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 587
ID ADB96920 standard; DNA; 172984 BP.
DE Human MDRI related DNA sequence SEQ ID NO:661.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 10; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 588
ID ADB92111 standard; DNA; 172984 BP.
DE Human MDRI related DNA sequence SEQ ID NO:661.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 10; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 589
ID ADO97167 standard; DNA; 176771 BP.
DE Human cancer associated sequence HD2-08-009, SEQ ID 143.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.8; DB 12; Length 176771;
Best Local Similarity 75.9%; Pred. No. 2.6e-46;
RESULT 590
ID ACN44418 standard; DNA; 213040 BP.
DE Human genomic sequence hCG41574.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 11; Length 213040;
Best Local Similarity 83.3%; Pred. No. 2.8e-46;
RESULT 591
ID AAH51601 standard; DNA; 319608 BP.
DE Human chromosome 13q31-q33 genomic nucleotide sequence.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 22.1%; Score 200.8; DB 3; Length 319608;
Best Local Similarity 84.7%; Pred. No. 3.3e-46;
RESULT 592
ID AAS09301 standard; DNA; 319608 BP.
DE Human schizophrenia associated gene q35030 and biallelic markers A1-A71.
Query Match 22.1%; Score 200.8; DB 5; Length 319608;
Best Local Similarity 84.7%; Pred. No. 3.3e-46;
RESULT 593
ID AAK84440 standard; DNA; 2821 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:39252.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 4; Length 2821;
Best Local Similarity 84.2%; Pred. No. 6.1e-47;
RESULT 594
ID AAS32797 standard; DNA; 5668 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 751.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 4; Length 5668;
Best Local Similarity 83.0%; Pred. No. 8e-47;
RESULT 595
ID AAK42719 standard; DNA; 8894 BP.
DE Genomic sequence #618 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 4; Length 8894;
Best Local Similarity 81.2%; Pred. No. 9.5e-47;
RESULT 596
ID ADB60875 standard; DNA; 8894 BP.
DE Connective tissue related genomic DNA #618.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMANA GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 9; Length 8894;
Best Local Similarity 81.2%; Pred. No. 9.5e-47;
RESULT 597
ID AAS36489 standard; DNA; 14902 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1703.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.6; DB 13; Length 14902;
Best Local Similarity 81.4%; Pred. No. 1.2e-46;
RESULT 598
ID ACN45210 standard; DNA; 48680 BP.
DE Human genomic sequence hCG37835.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.1% Score 200.6; DB 11; Length 48680;
Best Local Similarity 84.2%; Pred. No. 1.8e-46;
RESULT 599
ID ACA60949 standard; DNA; 55827 BP.
DE DNA encoding human carboxypeptidase.
PN US2003017574-A1.
Query Match 22.1% Score 200.6; DB 8; Length 55827;
Best Local Similarity 81.4%; Pred. No. 1.9e-46;
RESULT 600
ID ABX13671 standard; DNA; 55827 BP.
DE Human protease gene.
Query Match 22.1% Score 200.6; DB 10; Length 55827;
Best Local Similarity 81.4%; Pred. No. 1.9e-46;
RESULT 601
ID ADL27146 standard; DNA; 96593 BP.
DE Human genomic sequence for PPP3CC.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 22.1% Score 200.6; DB 11; Length 96593;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 602
ID ADA03068 standard; DNA; 96595 BP.
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1% Score 200.6; DB 9; Length 96595;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 603
ID ADB72806 standard; DNA; 96595 BP.
DE Human PPP3CC gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1% Score 200.6; DB 10; Length 96595;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 604
ID ADA6352 standard; DNA; 96596 BP.
DE Human PPP3CC gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1% Score 200.6; DB 9; Length 96596;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 605
ID ADJ7961 standard; DNA; 106344 BP.
DE Full length human glioma-associated oncogene-3 DNA, SEQ ID NO 10.
PN WO2003008549-A2.
PD 30-JAN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.1% Score 200.6; DB 11; Length 106344;
Best Local Similarity 85.5%; Pred. No. 2.5e-46;
RESULT 606
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1% Score 200.6; DB 11; Length 172569;
Best Local Similarity 79.4%; Pred. No. 3e-46;
RESULT 607
ID ABQ88207 standard; cDNA; 172570 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
PN WO2002050301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 22.1% Score 200.6; DB 6; Length 172570;
Best Local Similarity 80.3%; Pred. No. 3e-46;
RESULT 608
ID ADL13512 standard; DNA; 178870 BP.

DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003054166-A2.
PD 03-UTL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.1% Score 200.6; DB 10; Length 178870;
Best Local Similarity 83.0%; Pred. No. 3e-46;
RESULT 609
ID ACN44046 standard; DNA; 260027 BP.
DE Human genomic sequence hCG1735292.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1% Score 200.6; DB 11; Length 260027;
Best Local Similarity 83.0%; Pred. No. 3.5e-46;
RESULT 610
ID ABL41258 standard; cDNA; 1689 BP.
DE Human cytochrome bcl compound core protein II10.34 encoding cDNA.
PN CN1325876-A.
PD 12-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 22.1% Score 200.4; DB 6; Length 1689;
Best Local Similarity 77.9%; Pred. No. 5.7e-47;
RESULT 611
ID AAH15160 standard; cDNA; 1739 BP.
DE Human cDNA sequence SEQ ID NO:13234.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.1% Score 200.4; DB 4; Length 1739;
Best Local Similarity 83.7%; Pred. No. 5.8e-47;
RESULT 612
ID ABK69090 standard; cDNA; 2952 BP.
DE DNA encoding human secreted protein, SEQ ID NO 14.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1% Score 200.4; DB 6; Length 2952;
Best Local Similarity 78.2%; Pred. No. 7.1e-47;
RESULT 613
ID ADQ64569 standard; cDNA; 3341 BP.
DE Novel human cDNA sequence #1730.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.1% Score 200.4; DB 12; Length 3341;
Best Local Similarity 85.2%; Pred. No. 7.5e-47;
RESULT 614
ID ADJ78567 standard; DNA; 13278 BP.
DE Human cytochrome P450 isoenzyme 2D6 pseudogene Seg1D5.
PN WO2004009760-A2.
PD 29-JAN-2004.
PA (BIOV-) BIOVENTURES INC.
Query Match 22.1% Score 200.4; DB 12; Length 13278;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 615
ID ADM28895 standard; DNA; 13278 BP.
DE Human pseudogene #2 located near CYP2D6 gene.
PN US2004072235-A1.
PD 15-APR-2004.
PA (DAMS/) DAWSON E P.
Query Match 22.1% Score 200.4; DB 12; Length 13278;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 616
ID ADJ78568 standard; DNA; 13677 BP.
DE Human cytochrome P450 isoenzyme 2D6 pseudogene Seg1D6.
PN WO2004009760-A2.
PD 29-JAN-2004.
PA (BIOV-) BIOVENTURES INC.
Query Match 22.1% Score 200.4; DB 12; Length 13677;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 617
ID ADM28896 standard; DNA; 13677 BP.
DE Human pseudogene #3 located near CYP2D6 gene.

PN US2004072235-A1.
PD 15-APR-2004.
PA (DAMSON) E. P.
Query Match 22.1%; Score 200.4; DB 12; Length 13677;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 618
ID AAI62664 standard; DNA; 21936 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 314.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 619
ID AAL06758 standard; DNA; 21936 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9446.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 620
ID AAL06119 standard; DNA; 21936 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8807.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 621
ID ABL9684 standard; DNA; 21936 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3336.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 622
ID ABA15865 standard; DNA; 21936 BP.
DE Human nervous system related polynucleotide SEQ ID NO: 8196.
PN WO200155063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 5; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 623
ID AAI72317 standard; cDNA; 26657 BP.
DE Human transporter protein gene.
PN WO200202635-A2.
PD 10-JAN-2002.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.4; DB 6; Length 26657;
Best Local Similarity 80.9%; Pred. No. 1.7e-46;
RESULT 624
ID ABD32649 standard; DNA; 102790 BP.
DE Human cancer-associated genomic DNA HD13-036.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.4; DB 13; Length 102790;
Best Local Similarity 82.3%; Pred. No. 2.8e-46;
RESULT 625
ID ABD32811 standard; DNA; 161051 BP.
DE Human cancer-associated genomic DNA HD16-063.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.4; DB 13; Length 161051;
Best Local Similarity 85.2%; Pred. No. 3.3e-46;
RESULT 626
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.4; DB 11; Length 175077;
Best Local Similarity 82.3%; Pred. No. 3.4e-46;
RESULT 627
ID AAD58279 standard; DNA; 226475 BP.
DE Human tumour suppressor gene, Lmt reverse complement DNA.
PN WO2003066859-A1.
PD 14-AUG-2003.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELITZ.
Query Match 22.1%; Score 200.4; DB 9; Length 226475;
Best Local Similarity 81.1%; Pred. No. 3.8e-46;
RESULT 628
ID ABR83497 standard; cDNA; 227968 BP.
DE Human cDNA differentially expressed in granulocytic cells #68.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.1%; Score 200.4; DB 6; Length 227968;
Best Local Similarity 82.5%; Pred. No. 3.8e-46;
RESULT 629
ID ADQ18538 standard; DNA; 227968 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.1%; Score 200.4; DB 12; Length 227968;
Best Local Similarity 82.5%; Pred. No. 3.8e-46;
RESULT 630
ID ADS64405 standard; DNA; 601 BP.
DE Human transporter protein encoding gene fragment #11.
PN US2004151829-A1.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.2; DB 13; Length 601;
Best Local Similarity 81.1%; Pred. No. 4.4e-47;
RESULT 631
ID AAK71508 standard; DNA; 781 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 26320.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 781;
Best Local Similarity 80.7%; Pred. No. 4.9e-47;
RESULT 632
ID AAK71507 standard; DNA; 796 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 26319.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 796;
Best Local Similarity 80.7%; Pred. No. 4.9e-47;
RESULT 633
ID AAK86179 standard; DNA; 3341 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40991.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 3341;
Best Local Similarity 78.5%; Pred. No. 8.5e-47;
RESULT 634
ID AAK86178 standard; DNA; 3341 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40990.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 3341;
Best Local Similarity 78.5%; Pred. No. 8.5e-47;
RESULT 635
ID AAK85916 standard; DNA; 4553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40728.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 4553;
Best Local Similarity 83.2%; Pred. No. 9.6e-47;
RESULT 636
ID AAF97858 standard; DNA; 10709 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:72.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 22.1%; Score 200.2; DB 5; Length 10709;
Best Local Similarity 84.6%; Pred. No. 1.3e-46;
RESULT 637
ID AAF97857 standard; DNA; 13646 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:71.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 22.1%; Score 200.2; DB 5; Length 13646;
Best Local Similarity 84.6%; Pred. No. 1.5e-46;
RESULT 638
ID ABA15431 standard; DNA; 25012 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7762.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 5; Length 25012;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 639
ID AB273798 standard; DNA; 25012 BP.
DE Secreted protein gene 42 genomic fragment HBMTM1, SEQ ID NO:945.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 8; Length 25012;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 640
ID ADA88470 standard; DNA; 25012 BP.
DE Human secreted protein-related DNA sequence #63.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 8; Length 25012;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 641
ID ACN44118 standard; DNA; 31652 BP.
DE Human genomic sequence hCG23908.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.2; DB 11; Length 31652;
Best Local Similarity 70.8%; Pred. No. 2e-46;
RESULT 642
ID ADC87688 standard; DNA; 37138 BP.
DE Human mammalian target of rapamycin genomic fragment #33.
PN WO2003068350-A1.
PD 12-JUN-2003.
PA (NEMI-) NEM IND RES ORG.
Query Match 22.1%; Score 200.2; DB 10; Length 37138;
Best Local Similarity 79.1%; Pred. No. 2.2e-46;
RESULT 643
ID ADS36454 standard; DNA; 58337 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1668.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.2; DB 13; Length 58337;
Best Local Similarity 81.1%; Pred. No. 2.6e-46;
RESULT 644
ID ABD33260 standard; DNA; 59748 BP.
DE Human cancer-associated (CA) gene HD07-044.
PN WO2004058146-A2.

PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.2; DB 13; Length 59748;
Best Local Similarity 71.7%; Pred. No. 2.6e-46;
RESULT 645
ID ADS36462 standard; DNA; 64423 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1676.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.2; DB 13; Length 64423;
Best Local Similarity 81.1%; Pred. No. 2.7e-46;
RESULT 646
ID AAA10225 standard; DNA; 106746 BP.
DE Human PCTA-1 genomic DNA, SEQ ID NO:1.
PN WO9964590-A1.
PD 16-DEC-1999.
PA (GEST) GENSET.
Query Match 22.1%; Score 200.2; DB 3; Length 106746;
Best Local Similarity 83.2%; Pred. No. 3.2e-46;
RESULT 647
Query Match 22.1%; Score 200.2; DB 12; Length 110000;
Best Local Similarity 83.2%; Pred. No. 3.3e-46;
RESULT 648
ID ADA42607 standard; DNA; 113604 BP.
DE Human LQTS genomic DNA #2.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 22.1%; Score 200.2; DB 9; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 649
ID ADA42606 standard; DNA; 113604 BP.
DE Human LQTS genomic DNA #1.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 22.1%; Score 200.2; DB 9; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 650
ID ADS19853 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:1.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 22.1%; Score 200.2; DB 13; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 651
ID ADS19854 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:2.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 22.1%; Score 200.2; DB 13; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 652
ID AAC6548 standard; DNA; 121162 BP.
DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.
PN WO200063375-A1.
PD 26-OCT-2000.
PA (GEST) GENSET.
Query Match 22.1%; Score 200.2; DB 3; Length 121162;
Best Local Similarity 84.6%; Pred. No. 3.4e-46;
RESULT 653
ID ACN44966 standard; DNA; 125534 BP.
DE Human genomic sequence hCG32986.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.1%; Score 200.2; DB 11; Length 125534;
 Best Local Similarity 82.2%; Pred. No. 3.4e-46;
 RESULT 654
 ID ACN44142 standard; DNA; 143973 BP.
 DE Human genomic sequence hCG1546502.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200.2; DB 11; Length 143973;
 Best Local Similarity 78.5%; Pred. No. 3.6e-46;
 RESULT 655
 ID ABQ77400 standard; DNA; 174566 BP.
 DE Human ITGB3 DNA.
 PN WO2003016494-A2.
 PD 27-FEB-2003.
 PA (VITI-) VITIVITY INC.
 Query Match 22.1%; Score 200.2; DB 8; Length 174566;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 656
 ID ADL08118 standard; DNA; 174566 BP.
 DE Human gene associated with low HDL-C ITGB3.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match 22.1%; Score 200.2; DB 12; Length 174566;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 657
 ID ACN44650 standard; DNA; 256157 BP.
 DE Human genomic sequence hCG38672.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200.2; DB 11; Length 256157;
 Best Local Similarity 83.0%; Pred. No. 4.5e-46;
 RESULT 658
 ID ABD33570 standard; DNA; 256157 BP.
 DE Human cancer-associated (CA) gene HD07-114.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.1%; Score 200.2; DB 13; Length 256157;
 Best Local Similarity 83.0%; Pred. No. 4.5e-46;
 RESULT 659
 ID ADO26258 standard; DNA; 1061 BP.
 DE C35 promoter and polynucleotide targeting method related human DNA #1.
 PN WO2004037993-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M.
 PA (PARI/) PARIS M.
 Query Match 22.1%; Score 200; DB 12; Length 1061;
 Best Local Similarity 81.3%; Pred. No. 6.3e-47;
 RESULT 660
 ID ADO26269 standard; DNA; 1107 BP.
 DE Human breast cancer associated C35 promoter.
 PN WO2004037993-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M.
 PA (PARI/) PARIS M.
 Query Match 22.1%; Score 200; DB 12; Length 1107;
 Best Local Similarity 81.3%; Pred. No. 6.4e-47;
 RESULT 661
 ID ABQ83751 standard; cDNA; 1812 BP.
 DE Human nucleotide reductase 16.83 encoding cDNA SEQ ID NO:1.
 PN CN1347989-A.
 PD 08-MAY-2002.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 22.1%; Score 200; DB 6; Length 1812;
 Best Local Similarity 81.3%; Pred. No. 7.7e-47;
 RESULT 662
 ID ADO26370 standard; DNA; 7401 BP.
 DE C35 promoter and polynucleotide targeting method related human DNA #12.

PN WO2004037993-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M.
 PA (PARI/) PARIS M.
 Query Match 22.1%; Score 200; DB 12; Length 7401;
 Best Local Similarity 81.3%; Pred. No. 1.3e-46;
 RESULT 663
 ID AAK1538 standard; DNA; 8895 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 5114.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 4; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 664
 ID AA15795 standard; DNA; 8895 BP.
 DE Human colorectal cancer antigen coding sequence SEQ ID NO: 332.
 PN WO200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 4; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 665
 ID AAS3714 standard; DNA; 8895 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 668.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 4; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 666
 ID ABS9972 standard; DNA; 8895 BP.
 DE Genomic DNA #176 encoding human colorectal cancer related protein.
 PN US2002119919-A1.
 PD 29-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 22.1%; Score 200; DB 6; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 667
 ID ADB93125 standard; DNA; 8895 BP.
 DE Human colorectal cancer related polypeptide DNA #176.
 PN US2003054420-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 10; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 668
 ID ACC00503 standard; DNA; 23434 BP.
 DE Human histone deacetylase HDAC10 genomic DNA sequence, SEQ ID NO:4.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Query Match 22.1%; Score 200; DB 8; Length 23434;
 Best Local Similarity 78.1%; Pred. No. 2.1e-46;
 RESULT 669
 ID ADF90165 standard; DNA; 46649 BP.
 DE Genomic DNA encoding human transporter protein.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Query Match 22.1%; Score 200; DB 10; Length 46649;
 Best Local Similarity 79.1%; Pred. No. 2.7e-46;
 RESULT 670
 ID ADR03800 standard; DNA; 46649 BP.
 DE Human gene encoding a novel transporter.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Query Match 22.1%; Score 200; DB 13; Length 46649;
 Best Local Similarity 79.1%; Pred. No. 2.7e-46;
 RESULT 671
 ID ACN45002 standard; DNA; 60430 BP.
 DE Human genomic sequence hCG33210.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200; DB 11; Length 60430;
Best Local Similarity 80.9%; Pred. No. 3e-46;
RESULT 672
ID ABK94411 standard; DNA; 109906 BP.
DE DNA encoding endothelin converting enzyme 1 (ECE-1) #1.
PN WO200224747-A2.
PD 28-MAR-2002.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200; DB 6; Length 109906;
Best Local Similarity 85.4%; Pred. No. 3.7e-46;
RESULT 673
ID ADL08112 standard; DNA; 109906 BP.
DE Human gene associated with low HDL-C ECEL.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 22.1%; Score 200; DB 12; Length 109906;
Best Local Similarity 85.4%; Pred. No. 3.7e-46;
RESULT 674
ID ABD32806 standard; DNA; 653458 BP.
DE Human cancer-associated genomic DNA HD16-059.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200; DB 13; Length 110000;
Best Local Similarity 75.0%; Pred. No. 3.7e-46;
RESULT 675
ID ACN44334 standard; DNA; 161334 BP.
DE Human genomic sequence hCG32959.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200; DB 11; Length 161334;
Best Local Similarity 85.4%; Pred. No. 4.3e-46;
RESULT 676
ID ABD32688 standard; DNA; 208700 BP.
DE Human cancer-associated genomic DNA HD14-005.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200; DB 13; Length 208700;
Best Local Similarity 80.4%; Pred. No. 4.8e-46;
RESULT 677
ID ADL3684 standard; DNA; 247509 BP.
DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.1%; Score 200; DB 10; Length 247509;
Best Local Similarity 81.3%; Pred. No. 5.1e-46;
RESULT 678
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 22.1%; Score 200; DB 11; Length 304905;
Best Local Similarity 74.3%; Pred. No. 5.5e-46;
RESULT 679
ID AAA02015 standard; cDNA; 711 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2006.
PN WO9598675-A2.
PD 18-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.8; DB 3; Length 711;
Best Local Similarity 82.8%; Pred. No. 6.1e-47;
RESULT 680
ID AAL37239 standard; DNA; 2306 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3604.
PN WO200155367-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 2306;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 681
ID ABX60227 standard; cDNA; 2306 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2571.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.8; DB 8; Length 2306;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 682
ID ADJ30977 standard; DNA; 2306 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3604.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 12; Length 2306;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 683
ID AAL37240 standard; DNA; 2311 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3605.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 2311;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 684
ID ABX60228 standard; cDNA; 2311 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2572.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.8; DB 8; Length 2311;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 685
ID ADJ30978 standard; DNA; 2311 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3605.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 12; Length 2311;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 686
ID AAL37241 standard; DNA; 2312 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3606.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 2312;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 687
ID ABX60229 standard; cDNA; 2312 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2573.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.8; DB 8; Length 2312;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 688
ID ADJ30979 standard; DNA; 2312 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3606.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 12; Length 2312;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;

RESULT 689
 ID ADO4272 standard; DNA; 3364 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7092.
 PN WO2004068938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 3364;
 Best Local Similarity 80.9%; Pred. No. 1.1e-46;
 RESULT 690
 ID AAI61061 standard; cDNA; 3775 BP.
 DE Human polynucleotide SEQ ID NO 5050.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 3775;
 Best Local Similarity 83.3%; Pred. No. 1.2e-46;
 RESULT 691
 ID AAK74057 standard; DNA; 5024 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28869.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 5024;
 Best Local Similarity 83.4%; Pred. No. 1.3e-46;
 RESULT 692
 ID AAK74056 standard; DNA; 5024 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28868.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 5024;
 Best Local Similarity 83.4%; Pred. No. 1.3e-46;
 RESULT 693
 ID ADC86878 standard; DNA; 10102 BP.
 DE Human GPCR gene SEQ ID NO:1331.
 PN EPI270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATOR.
 Query Match 22.0%; Score 199.8; DB 10; Length 10102;
 Best Local Similarity 86.2%; Pred. No. 1.7e-46;
 RESULT 694
 ID AAS27797 standard; DNA; 18449 BP.
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1457.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 18449;
 Best Local Similarity 80.9%; Pred. No. 2.1e-46;
 RESULT 695
 ID ABA20913 standard; DNA; 18449 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13244.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 5; Length 18449;
 Best Local Similarity 80.9%; Pred. No. 2.1e-46;
 RESULT 696
 ID ADB94600 standard; DNA; 18449 BP.
 DE Novel human protein DNA #209.
 PN US2002168711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.
 Query Match 22.0%; Score 199.8; DB 10; Length 18449;
 Best Local Similarity 80.9%; Pred. No. 2.1e-46;
 RESULT 697
 ID ACN44810 standard; DNA; 25668 BP.
 DE Human genomic sequence hc28332.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.0%; Score 199.8; DB 11; Length 25668;
 Best Local Similarity 80.9%; Pred. No. 2.4e-46;
 RESULT 698
 ID ABA07160 standard; DNA; 31931 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 479.
 PN WO200155206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 31931;
 Best Local Similarity 83.3%; Pred. No. 2.6e-46;
 RESULT 699
 ID ADC20666 standard; DNA; 51961 BP.
 DE Human secreted protein-related DNA sequence #84.
 PN WO200292787-A2.
 PD 21-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 10; Length 51961;
 Best Local Similarity 83.3%; Pred. No. 3.2e-46;
 RESULT 700
 ID ABT16905 standard; DNA; 51961 BP.
 DE Human secreted protein-related DNA sequence - SEQ ID NO 259.
 PN WO200277188-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 10; Length 51961;
 Best Local Similarity 83.3%; Pred. No. 3.2e-46;
 RESULT 701
 ID ABZ67488 standard; DNA; 51961 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1011.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 10; Length 51961;
 Best Local Similarity 83.3%; Pred. No. 3.2e-46;
 RESULT 702
 ID ADE95902 standard; DNA; 94720 BP.
 DE Human STR5B gene genomic DNA sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.8; DB 10; Length 94720;
 Best Local Similarity 81.1%; Pred. No. 4e-46;
 RESULT 703
 ID ADA02654 standard; DNA; 94720 BP.
 DE Human STR5B carcinoma associated gene, SEQ ID NO:1172.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.8; DB 9; Length 94720;
 Best Local Similarity 81.1%; Pred. No. 4e-46;
 RESULT 704
 ID ADB72392 standard; DNA; 94720 BP.
 DE Human STR5B gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.8; DB 10; Length 94720;
 Best Local Similarity 81.1%; Pred. No. 4e-46;
 RESULT 705
 ID ADQ97846 standard; DNA; 94911 BP.
 DE Human cancer associated sequence HD11-010, SEQ ID 823.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 94911;
 Best Local Similarity 79.7%; Pred. No. 4e-46;
 RESULT 706
 ID ADN06353 standard; DNA; 398800 BP.
 DE Human FLAP genomic DNA SEQ ID NO:1.
 PN WO2004035741-A2.
 PD 29-APR-2004.
 PA (DECO-) DECODE GENETICS BHF.
 Query Match 22.0%; Score 199.8; DB 12; Length 110000;

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Best Local Similarity 80.9%; Pred. No. 4.3e-46;
RESULT 707
ID ADS94372 standard; DNA; 398800 BP.
DE Human 5-lipoxygenase activating protein (FLAP) gene.
PN WO2004035746-A2.
PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 22.0%; Score 199.8; DB 13; Length 110000;
Best Local Similarity 80.9%; Pred. No. 4.3e-46;
RESULT 708
ID ACN44026 standard; DNA; 122923 BP.
DE Human genomic sequence hCG24510.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 11; Length 122923;
Best Local Similarity 80.9%; Pred. No. 4.5e-46;
RESULT 709
ID ADQ21602 standard; DNA; 131673 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4422.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 131673;
Best Local Similarity 84.6%; Pred. No. 4.6e-46;
RESULT 710
ID ADQ9369 standard; DNA; 155937 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 155937;
Best Local Similarity 83.0%; Pred. No. 4.9e-46;
RESULT 711
ID AAD02697 standard; DNA; 160552 BP.
DE Human glycosyl sulfoxyltransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (RESC-) UNIV CALIFORNIA.
Query Match 22.0%; Score 199.8; DB 4; Length 160552;
Best Local Similarity 76.7%; Pred. No. 4.9e-46;
RESULT 712
ID ABD33314 standard; DNA; 170489 BP.
DE Human cancer-associated (CA) gene HD07-056.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.8; DB 13; Length 170489;
Best Local Similarity 80.9%; Pred. No. 5.1e-46;
RESULT 713
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 11; Length 174448;
Best Local Similarity 82.0%; Pred. No. 5.1e-46;
RESULT 714
ID ADE09750 standard; DNA; 1608 BP.
DE Novel DNA-related contig nucleotide sequence #472.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 10; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 715
ID ADS11591 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1828.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 716
ID ADS11592 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1829.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 717
ID ADS11590 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1827.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 718
ID ADS1159 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1396.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 719
ID AAK94819 standard; cDNA; 1748 BP.
DE Human full-length cDNA, SEQ ID NO: 3960.
PN EP130084-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.0%; Score 199.6; DB 4; Length 1748;
Best Local Similarity 84.1%; Pred. No. 9.9e-47;
RESULT 720
ID AD131927 standard; cDNA; 1748 BP.
DE Full length human cDNA clone SeqID 3960.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.6; DB 12; Length 1748;
Best Local Similarity 84.1%; Pred. No. 9.9e-47;
RESULT 721
ID ADA52479 standard; cDNA; 2261 BP.
DE Human coding sequence, SEQ ID 47.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 22.0%; Score 199.6; DB 10; Length 2261;
Best Local Similarity 84.1%; Pred. No. 1.1e-46;
RESULT 722
ID AAI59666 standard; cDNA; 2982 BP.
DE Human polynucleotide SEQ ID NO 3655.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 4; Length 2982;
Best Local Similarity 84.1%; Pred. No. 1.2e-46;
RESULT 723
ID ABK69113 standard; cDNA; 3047 BP.
DE DNA encoding human secreted protein, SEQ ID NO 37.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 6; Length 3047;
Best Local Similarity 84.1%; Pred. No. 1.2e-46;
RESULT 724
ID AAI57880 standard; cDNA; 3262 BP.
DE Human polynucleotide SEQ ID NO 83.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 4; Length 3262;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
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RESULT 725
ID ADO67504 standard; cDNA; 3660 BP.
DE Novel human cDNA sequence #2477.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.6; DB 12; Length 3660;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
RESULT 726
ID ABO75955 standard; cDNA; 3716 BP.
DE Human PMM encoding sequence Incyte ID 7972712CB1.
PN WO200246383-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.0%; Score 199.6; DB 6; Length 3716;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
RESULT 727
ID ABK83341 standard; cDNA; 4037 BP.
DE cDNA encoding human DPRP-2 splice variant #9.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4037;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 728
ID ABK83337 standard; cDNA; 4076 BP.
DE cDNA encoding human DPRP-2 splice variant #5.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4076;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 729
ID ABK83340 standard; cDNA; 4120 BP.
DE cDNA encoding human DPRP-2 splice variant #8.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4120;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 730
ID ADO86753 standard; cDNA; 4147 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3628.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GERTH-) GENENTECH INC.
PA (WUTD-) WU T D.
PA (ZHOU-) ZHOU Y.
Query Match 22.0%; Score 199.6; DB 12; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 731
ID ADO84273 standard; cDNA; 4147 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1087.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GERTH-) GENENTECH INC.
PA (WUTD-) WU T D.
PA (ZHOU-) ZHOU Y.
Query Match 22.0%; Score 199.6; DB 13; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 732
ID ACN440423 standard; cDNA; 4147 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA26538, SEQ ID NO:5194.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH-) GENENTECH INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 733
ID ABK83336 standard; cDNA; 4159 BP.
DE cDNA encoding human DPRP-2 splice variant #4.
PN WO200231134-A2.
PD 18-APR-2002.
PA (HOMA-) HUMAN GENOME SCI INC.

PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4159;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 734
ID ABK83339 standard; cDNA; 4180 BP.
DE cDNA encoding human DPRP-2 splice variant #7.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4180;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 735
ID ABK83335 standard; cDNA; 4219 BP.
DE cDNA encoding human DPRP-2 splice variant #3.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4219;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 736
ID ABK83338 standard; cDNA; 4263 BP.
DE cDNA encoding human DPRP-2 splice variant #6.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4263;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 737
ID ADS10268 standard; DNA; 4284 BP.
DE Human therapeutic DNA - SEQ ID 505.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4284;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 738
ID ABK83333 standard; cDNA; 4302 BP.
DE cDNA encoding human DPRP-2 splice variant #1.
PN WO200231134-A2.
PD 18-APR-2002.
PA (PERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4302;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 739
ID ADS10269 standard; DNA; 4359 BP.
DE Human therapeutic DNA - SEQ ID 506.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4359;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 740
ID ADS10267 standard; DNA; 4398 BP.
DE Human therapeutic DNA - SEQ ID 504.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4398;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 741
ID AAK79131 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33943.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 14216;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
RESULT 742
ID AAK79133 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33945.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HOMA-) HUMAN GENOME SCI INC.

Query Match 22.0%; Score 199.6; DB 4; Length 14216;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
RESULT 743
ID AAS41759 standard; DNA; 22428 BP.
DE Genomic sequence #75 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 744
ID ABZ74201 standard; DNA; 22428 BP.
DE secreted protein gene 215 genomic fragment HNGAMS8, SEQ ID NO:1348.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 8; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 745
ID ADA98730 standard; DNA; 22428 BP.
DE Human secreted protein-related DNA sequence #323.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 8; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 746
ID ABZ67767 standard; DNA; 22428 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1290.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 10; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 747
ID AAK61763 standard; DNA; 37959 BP.
DE Humane immune/haematopoietic antigen genomic sequence SEQ ID NO:36575.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 37959;
Best Local Similarity 82.8%; Pred. No. 3.2e-46;
RESULT 748
ID ACN44818 standard; DNA; 116704 BP.
DE Human genomic sequence hCG30155.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.6; DB 11; Length 116704;
Best Local Similarity 82.9%; Pred. No. 5e-46;
RESULT 749
ID ADP60536 standard; DNA; 118788 BP.
DE Human HPC2/ELAC2 gene SeqID1.
PN JP200416565-A.
PD 17-JUN-2004.
PA (TAKA/) TAKAHASHI H.
PA (WATA/) WATANABE M.
PA (FURU/) FURUSATO M.
PA (HONS) YAKULT HONSHA KK.
Query Match 22.0%; Score 199.6; DB 12; Length 118788;
Best Local Similarity 82.8%; Pred. No. 5e-46;
RESULT 750
ID ABD33219 standard; DNA; 135827 BP.
DE Human cancer-associated (CA) gene HD07-035.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.6; DB 13; Length 135827;
Best Local Similarity 78.6%; Pred. No. 5.3e-46;
RESULT 751
ID ABD32612 standard; DNA; 142976 BP.
DE Human cancer-associated genomic DNA HD12-017.
PN WO2004074320-A2.

PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.6; DB 13; Length 142976;
Best Local Similarity 83.1%; Pred. No. 5.4e-46;
RESULT 752
ID ACN44374 standard; DNA; 181684 BP.
DE Human genomic sequence hCG16651.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.6; DB 11; Length 181684;
Best Local Similarity 82.8%; Pred. No. 5.9e-46;
RESULT 753
ID AAH92610 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR1310a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.
PA (ELIT-) ELIIPSIS BIOTHERAPEUTICS CORP.
Query Match 22.0%; Score 199.4; DB 4; Length 700;
Best Local Similarity 81.1%; Pred. No. 7.9e-47;
RESULT 754
ID AAL36476 standard; DNA; 1664 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2841.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 4; Length 1664;
Best Local Similarity 86.4%; Pred. No. 1.1e-46;
RESULT 755
ID ABX59464 standard; cDNA; 1664 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1808.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.4; DB 8; Length 1664;
Best Local Similarity 86.4%; Pred. No. 1.1e-46;
RESULT 756
ID ADJ30214 standard; DNA; 1664 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2841.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 12; Length 1664;
Best Local Similarity 86.4%; Pred. No. 1.1e-46;
RESULT 757
ID ADM03474 standard; cDNA; 1756 BP.
DE Human cDNA of the invention SEQ ID NO:2159.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.4; DB 11; Length 1756;
Best Local Similarity 82.4%; Pred. No. 1.1e-46;
RESULT 758
ID ABK92513 standard; DNA; 6096 BP.
DE Human prostate specific nucleic acid #132.
PN WO200238810-A2.
PD 16-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 22.0%; Score 199.4; DB 6; Length 6096;
Best Local Similarity 76.0%; Pred. No. 1.8e-46;
RESULT 759
ID AAS42014 standard; DNA; 6437 BP.
DE Genomic sequence #330 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 4; Length 6437;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 760
ID AAK69231 standard; DNA; 8658 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24043.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.4; DB 4; Length 8658;
 Best Local Similarity 81.1%; Pred. No. 2.1e-46;
 RESULT 761
 ID AAS42015 standard; DNA; 9742 BP.
 DE Genomic sequence #331 encoding novel human enzyme polypeptide.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.4; DB 4; Length 9742;
 Best Local Similarity 81.1%; Pred. No. 2.2e-46;
 RESULT 762
 ID ACN44990 standard; DNA; 33317 BP.
 DE Human genomic sequence hCG27461.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.4; DB 11; Length 33317;
 Best Local Similarity 81.3%; Pred. No. 3.5e-46;
 RESULT 763
 ID AAD44995 standard; DNA; 49984 BP.
 DE Human transporter genomic DNA.
 Query Match 22.0%; Score 199.4; DB 6; Length 49984;
 Best Local Similarity 81.1%; Pred. No. 4.1e-46;
 RESULT 764
 ID ADS64392 standard; DNA; 49984 BP.
 DE Human transporter protein encoding gene.
 Query Match 22.0%; Score 199.4; DB 13; Length 49984;
 Best Local Similarity 81.1%; Pred. No. 4.1e-46;
 RESULT 765
 ID AAL53466 standard; DNA; 70372 BP.
 DE Ras-like protein genomic DNA.
 Query Match 22.0%; Score 199.4; DB 6; Length 70372;
 Best Local Similarity 81.1%; Pred. No. 4.7e-46;
 RESULT 766
 ID ADQ97870 standard; DNA; 121160 BP.
 DE Human cancer associated sequence HD11-015, SEQ ID 847.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.4; DB 12; Length 121160;
 Best Local Similarity 76.0%; Pred. No. 5.8e-46;
 RESULT 767
 ID ADH19244 standard; DNA; 124164 BP.
 DE Human 5-hydroxytryptamine receptor type 3B SNP variant DNA.
 PN WO2003097873-A2.
 PD 27-NOV-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 22.0%; Score 199.4; DB 12; Length 124164;
 Best Local Similarity 81.1%; Pred. No. 5.8e-46;
 RESULT 768
 ID ADH19246 standard; DNA; 124165 BP.
 DE Human 5-hydroxytryptamine receptor type 3B SNP variant DNA 2.
 PN WO2003097873-A2.
 PD 27-NOV-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 22.0%; Score 199.4; DB 12; Length 124165;
 Best Local Similarity 81.1%; Pred. No. 5.8e-46;
 RESULT 769
 ID ADP83402 standard; DNA; 124167 BP.
 DE Human 5-hydroxytryptamine receptor type 3 gene.
 PN WO2003100091-A1.
 PD 04-DEC-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 22.0%; Score 199.4; DB 12; Length 124167;
 Best Local Similarity 81.1%; Pred. No. 5.8e-46;
 RESULT 770
 ID ADH19240 standard; DNA; 124167 BP.
 DE Human 5-hydroxytryptamine receptor type 3B gDNA.
 PN WO2003097873-A2.

PD 27-NOV-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 22.0%; Score 199.4; DB 12; Length 124167;
 Best Local Similarity 81.1%; Pred. No. 5.8e-46;
 RESULT 771
 ID ADQ97301 standard; DNA; 127722 BP.
 DE Human cancer associated sequence HD08-028, SEQ ID 278.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.4; DB 12; Length 127722;
 Best Local Similarity 81.5%; Pred. No. 5.9e-46;
 RESULT 772
 ID AAD55538 standard; DNA; 133893 BP.
 DE Human phosphatidylinositol diphosphate (PIB) DNA #1.
 PN WO200299125-A1.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 22.0%; Score 199.4; DB 9; Length 133893;
 Best Local Similarity 78.9%; Pred. No. 6e-46;
 RESULT 773
 ID ADL13638 standard; DNA; 186528 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #170.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.0%; Score 199.4; DB 10; Length 186528;
 Best Local Similarity 79.9%; Pred. No. 6.8e-46;
 RESULT 774
 ID ABD32598 standard; DNA; 290547 BP.
 DE Human cancer-associated genomic DNA HD7-220.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.4; DB 13; Length 290547;
 Best Local Similarity 81.1%; Pred. No. 8.1e-46;
 RESULT 775
 ID AAX61843 standard; DNA; 601 BP.
 DE Novel human transporter protein related polynucleotide #39.
 PN US2002142381-A1.
 PD 03-OCT-2002.
 PA (GONG/) GONG F.
 PA (KERC/) KENCHIM K A.
 PA (OPRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 22.0%; Score 199.2; DB 8; Length 601;
 Best Local Similarity 76.7%; Pred. No. 8.5e-47;
 RESULT 776
 ID AAK80126 standard; DNA; 4115 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34938.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.2; DB 4; Length 4115;
 Best Local Similarity 84.6%; Pred. No. 1.8e-46;
 RESULT 777
 ID ABQ78002 standard; DNA; 21222 BP.
 DE Human transporter protein encoding genomic DNA SEQ ID NO 3.
 Query Match 22.0%; Score 199.2; DB 6; Length 21222;
 Best Local Similarity 80.6%; Pred. No. 3.4e-46;
 RESULT 778
 ID AAK89418 standard; DNA; 28588 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 2994.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.2; DB 4; Length 28588;
 Best Local Similarity 82.8%; Pred. No. 3.6e-46;
 RESULT 779
 ID AAS31923 standard; DNA; 28588 BP.
 DE Human liver associated genomic DNA #97.
 PN WO200155315-A1.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.2; DB 5; Length 28588;
 Best Local Similarity 82.8%; Pred. No. 3.8e-46;
 RESULT 780
 ID ABRN90278 standard; DNA; 28588 BP.
 DE Human liver antigen HLDRI94 genomic sequence, SEQ ID NO:399.
 PN US2002042096-A1.
 PD 11-APR-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 22.0%; Score 199.2; DB 6; Length 28588;
 Best Local Similarity 82.8%; Pred. No. 3.8e-46;
 RESULT 781
 ID ADU15191 standard; DNA; 28588 BP.
 DE Human liver-related genomic DNA - SEQ ID 399.
 PN US2003077602-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.2; DB 11; Length 28588;
 Best Local Similarity 82.8%; Pred. No. 3.8e-46;
 RESULT 782
 ID ABR87217 standard; DNA; 30709 BP.
 DE Human lipase, hormone-sensitive (LIPe) gene sequence.
 Query Match 22.0%; Score 199.2; DB 6; Length 30709;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 783
 ID ABD3578 standard; DNA; 43853 BP.
 DE Human cancer-associated (CA) gene HD07-116.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.2; DB 13; Length 43853;
 Best Local Similarity 80.6%; Pred. No. 4.5e-46;
 RESULT 784
 ID ACN4386 standard; DNA; 61103 BP.
 DE Human genomic sequence hCG1784975.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.2; DB 11; Length 61103;
 Best Local Similarity 81.9%; Pred. No. 5.1e-46;
 RESULT 785
 ID ACN44230 standard; DNA; 66973 BP.
 DE Human genomic sequence hCG21559.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.2; DB 11; Length 66973;
 Best Local Similarity 84.4%; Pred. No. 5.2e-46;
 RESULT 786
 ID ADQ97968 standard; DNA; 78082 BP.
 DE Human cancer associated sequence HD11-032, SEQ ID 945.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.2; DB 12; Length 78082;
 Best Local Similarity 82.8%; Pred. No. 5.6e-46;
 RESULT 787
 Query Match 22.0%; Score 199.2; DB 13; Length 88759;
 Best Local Similarity 80.1%; Pred. No. 5.8e-46;
 RESULT 788
 ID ADH56439 standard; DNA; 95001 BP.
 DE Human hypothetical tumour endothelial marker DNA.
 PN US2003232770-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 22.0%; Score 199.2; DB 12; Length 95001;
 Best Local Similarity 80.6%; Pred. No. 6e-46;
 RESULT 789
 ID ADC85301 standard; DNA; 96591 BP.
 DE Mouse Sox1 coding sequence.
 PN WO2003045230-A2.

PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.2; DB 10; Length 96591;
 Best Local Similarity 76.0%; Pred. No. 6e-46;
 RESULT 790
 ID ADA02822 standard; DNA; 96592 BP.
 DE Human S0S1 carcinoma associated gene, SEQ ID NO:1340.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.2; DB 9; Length 96592;
 Best Local Similarity 76.0%; Pred. No. 6e-46;
 RESULT 791
 ID ADB72560 standard; DNA; 96592 BP.
 DE Human S0S1 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.2; DB 10; Length 96592;
 Best Local Similarity 76.0%; Pred. No. 6e-46;
 RESULT 792
 ID ADM74417 standard; DNA; 96592 BP.
 DE Human carcinoma associated (CA) nucleic acid #43.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORE/) MORRIS D W.
 PA (ENGE/) ENGELHARD E K.
 Query Match 22.0%; Score 199.2; DB 12; Length 96592;
 Best Local Similarity 76.0%; Pred. No. 6e-46;
 RESULT 793
 ID ADS36461 standard; DNA; 158417 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 22.0%; Score 199.2; DB 13; Length 158417;
 Best Local Similarity 85.1%; Pred. No. 7.3e-46;
 RESULT 794
 ID AAH13291 standard; cDNA; 559 BP.
 DE Human cDNA clone (3'-primer) SEQ ID NO:10126.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 21.9%; Score 199; DB 4; Length 559;
 Best Local Similarity 83.8%; Pred. No. 9.5e-47;
 RESULT 795
 ID AAK72518 standard; DNA; 2502 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27330.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 199; DB 4; Length 2502;
 Best Local Similarity 85.1%; Pred. No. 1.7e-46;
 RESULT 796
 ID AAK70822 standard; DNA; 3371 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25634.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 199; DB 4; Length 3371;
 Best Local Similarity 78.0%; Pred. No. 1.9e-46;
 RESULT 797
 ID ADQ64845 standard; cDNA; 4634 BP.
 DE Novel human cDNA sequence #2006.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
 Query Match 21.9%; Score 199; DB 12; Length 4634;
 Best Local Similarity 85.1%; Pred. No. 2.1e-46;
 RESULT 798
 ID ABA20857 standard; DNA; 11234 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13188.
 PN WO200159063-A2.

PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 5; Length 11234;
Best Local Similarity 81.3%; Pred. No. 3e-46;
RESULT 799
ID ABK49701 standard; DNA; 32816 BP.
DE Human transporter protein genomic DNA sequence.
Query Match 21.9%; Score 199; DB 6; Length 32816;
Best Local Similarity 85.1%; Pred. No. 4.5e-46;
RESULT 800
ID ADG16994 standard; DNA; 32816 BP.
DE Human transporter protein DNA.
Query Match 21.9%; Score 199; DB 12; Length 32816;
Best Local Similarity 85.1%; Pred. No. 4.5e-46;
RESULT 801
ID ABX13675 standard; DNA; 33239 BP.
DE Human secreted protein gene.
PN US2002137130-A1.
PD 26-SEP-2002.
PA (WEIM/) WEI M.
PA (GONG/) GONG F.
PA (DEPA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 21.9%; Score 199; DB 8; Length 33239;
Best Local Similarity 81.5%; Pred. No. 4.6e-46;
RESULT 802
ID AAK74751 standard; DNA; 36485 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29563.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 4; Length 36485;
Best Local Similarity 80.1%; Pred. No. 4.7e-46;
RESULT 803
ID AAK68958 standard; DNA; 36485 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23770.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 4; Length 36485;
Best Local Similarity 80.1%; Pred. No. 4.7e-46;
RESULT 804
ID AAD48290 standard; DNA; 39982 BP.
DE Human enzyme protein encoding gene.
Query Match 21.9%; Score 199; DB 8; Length 39982;
Best Local Similarity 85.1%; Pred. No. 4.9e-46;
RESULT 805
ID ABD32585 standard; DNA; 50927 BP.
DE Human cancer-associated genomic DNA HD7-210.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 199; DB 13; Length 50927;
Best Local Similarity 85.1%; Pred. No. 5.4e-46;
RESULT 806
ID ADO97599 standard; DNA; 106130 BP.
DE Human cancer associated sequence HD10-012, SEQ ID 576.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 199; DB 12; Length 106130;
Best Local Similarity 85.1%; Pred. No. 7.1e-46;
RESULT 807
Query Match 21.9%; Score 199; DB 11; Length 110000;
Best Local Similarity 85.1%; Pred. No. 7.2e-46;
RESULT 808
ID ACN44602 standard; DNA; 126266 BP.
DE Human genomic sequence hCG1781402.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 199; DB 11; Length 126266;
Best Local Similarity 81.5%; Pred. No. 7.6e-46;

RESULT 809
ID ADH63063 standard; DNA; 132762 BP.
DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
PN WO2003024987-A1.
PD 27-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.9%; Score 199; DB 10; Length 132762;
Best Local Similarity 81.5%; Pred. No. 7.8e-46;
RESULT 810
ID ADP45594 standard; DNA; 133100 BP.
DE Human NTM91/FLJ20625/LOC220074 region gDNA.
Query Match 21.9%; Score 199; DB 12; Length 133100;
Best Local Similarity 81.5%; Pred. No. 7.8e-46;
RESULT 811
ID ACA62841 standard; DNA; 148567 BP.
DE Human kinase DNA.
Query Match 21.9%; Score 199; DB 9; Length 148567;
Best Local Similarity 79.3%; Pred. No. 8.1e-46;
RESULT 812
ID ABS55500 standard; DNA; 148567 BP.
DE Gene encoding human serine/threonine protein kinase-like kinase.
Query Match 21.9%; Score 199; DB 10; Length 148567;
Best Local Similarity 79.3%; Pred. No. 8.1e-46;
RESULT 813
ID ADL09163 standard; DNA; 148567 BP.
DE Human protein kinase, genomic DNA.
Query Match 21.9%; Score 199; DB 12; Length 148567;
Best Local Similarity 79.3%; Pred. No. 8.1e-46;
RESULT 814
ID ACP62741 standard; DNA; 189013 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:669.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 8; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 815
ID ADB20856 standard; DNA; 189013 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:669.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 8; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 816
ID ADB87945 standard; DNA; 189013 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:669.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 10; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 817
ID ADB96928 standard; DNA; 189013 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:669.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 10; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 818
ID ADB92119 standard; DNA; 189013 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:669.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 10; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 819
ID ACN44170 standard; DNA; 196686 BP.
DE Human genomic sequence hCG39530.
PN WO2003073826-A2.
PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 199; DB 11; Length 196686;
Best Local Similarity 81.3%; Pred. No. 9.1e-46;
RESULT 820
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (MAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 21.9%; Score 199; DB 10; Length 349989;
Best Local Similarity 78.5%; Pred. No. 1.1e-45;
RESULT 821
ID ABN62834 standard; cDNA; 402 BP.
DE Human cancer related polynucleotide SEQ ID NO 2801.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.8; DB 6; Length 402;
Best Local Similarity 79.6%; Pred. No. 9.5e-47;
RESULT 822
ID AAK75637 standard; DNA; 2173 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30449.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 2173;
Best Local Similarity 75.2%; Pred. No. 1.8e-46;
RESULT 823
ID AAH16224 standard; cDNA; 2591 BP.
DE Human cDNA sequence SEQ ID NO:15042.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 21.9%; Score 198.8; DB 4; Length 2591;
Best Local Similarity 81.8%; Pred. No. 2e-46;
RESULT 824
ID ADL22885 standard; DNA; 2591 BP.
DE Human WP2153 coding sequence SEQ ID NO: 5.
PN WO2004015069-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 21.9%; Score 198.8; DB 12; Length 2591;
Best Local Similarity 81.8%; Pred. No. 2e-46;
RESULT 825
ID ADRI4082 standard; DNA; 2591 BP.
DE Human NF-kappaB pathway-associated gene SeqID83.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 21.9%; Score 198.8; DB 13; Length 2591;
Best Local Similarity 81.8%; Pred. No. 2e-46;
RESULT 826
ID ADRO8024 standard; cDNA; 3385 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1530.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.8; DB 13; Length 3385;
Best Local Similarity 85.9%; Pred. No. 2.2e-46;
RESULT 827
ID ACN37218 standard; DNA; 20001 BP.
DE Human periodontal disease related gene PTCDS SEQ ID NO:128.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KAMO/) KAMO K.
Query Match 21.9%; Score 198.8; DB 13; Length 20001;
Best Local Similarity 83.0%; Pred. No. 4.3e-46;
RESULT 828
ID AAK81266 standard; DNA; 21458 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36078.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21458;
Best Local Similarity 82.1%; Pred. No. 4.4e-46;
RESULT 829
ID AAL06122 standard; DNA; 21458 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8810.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21458;
Best Local Similarity 82.1%; Pred. No. 4.4e-46;
RESULT 830
ID ABL98687 standard; DNA; 21458 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3339.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21458;
Best Local Similarity 82.1%; Pred. No. 4.4e-46;
RESULT 831
ID ABK42270 standard; DNA; 21470 BP.
DE Genomic sequence #169 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21470;
Best Local Similarity 83.0%; Pred. No. 4.4e-46;
RESULT 832
ID ADB60426 standard; DNA; 21470 BP.
DE Connective tissue related genomic DNA #169.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 9; Length 21470;
Best Local Similarity 83.0%; Pred. No. 4.4e-46;
RESULT 833
ID ADA02702 standard; DNA; 21666 BP.
DE Human Nuprl carcinoma associated gene, SEQ ID NO:1220.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 9; Length 21666;
Best Local Similarity 84.9%; Pred. No. 4.4e-46;
RESULT 834
ID ADB72440 standard; DNA; 21666 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 10; Length 21666;
Best Local Similarity 84.9%; Pred. No. 4.4e-46;
RESULT 835
ID ADB95950 standard; DNA; 21666 BP.
DE Human hCG1745228 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 10; Length 21666;
Best Local Similarity 84.9%; Pred. No. 4.4e-46;
RESULT 836
ID ADK40307 standard; DNA; 23469 BP.
DE Human HNF1alpha gene SEQ ID NO:27.
PN WO2004016813-A2.
PD 26-FEB-2004.
PA (INEM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 21.9%; Score 198.8; DB 12; Length 23469;
Best Local Similarity 77.3%; Pred. No. 4.6e-46;
RESULT 837
ID ACN37244 standard; DNA; 25382 BP.
DE Human periodontal disease related gene IL4R SEQ ID NO:154.
Query Match 21.9%; Score 198.8; DB 13; Length 25382;

Best Local Similarity 82.1%; Pred. No. 4.7e-46;
RESULT 838
ID AAF57718 standard; DNA; 28690 BP.
DE Human IL4RaIpha gene.
PN WO200104270-A1.
PD 18-JAN-2001.
PA (GENA-) GENMISANCE PHARM INC.
Query Match 21.9%; Score 198.8; DB 5; Length 28690;
Best Local Similarity 82.1%; Pred. No. 4.9e-46;
RESULT 839
ID ADS36474 standard; DNA; 40947 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.8; DB 13; Length 40947;
Best Local Similarity 79.7%; Pred. No. 5.7e-46;
RESULT 840
ID AAK6531 standard; DNA; 41159 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20443.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 41159;
Best Local Similarity 81.2%; Pred. No. 5.7e-46;
RESULT 841
ID AAD36022 standard; DNA; 43950 BP.
DE Human kinase genomic DNA.
Query Match 21.9%; Score 198.8; DB 6; Length 43950;
Best Local Similarity 81.2%; Pred. No. 5.8e-46;
RESULT 842
ID AAD33486 standard; DNA; 51289 BP.
DE Human cancer-associated (CA) gene HD07-094.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.8; DB 13; Length 51289;
Best Local Similarity 86.2%; Pred. No. 6.2e-46;
RESULT 843
ID ABD33339 standard; DNA; 62658 BP.
DE Human cancer-associated (CA) gene HD07-061.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.8; DB 13; Length 62658;
Best Local Similarity 81.2%; Pred. No. 6.7e-46;
RESULT 844
ID ACN44522 standard; DNA; 70779 BP.
DE Human genomic sequence hCG17357.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 11; Length 70779;
Best Local Similarity 82.1%; Pred. No. 7e-46;
RESULT 845
ID ABI64158 standard; DNA; 84539 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2495.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 21.9%; Score 198.8; DB 6; Length 84539;
Best Local Similarity 75.6%; Pred. No. 7.5e-46;
RESULT 846
ID ADU13479 standard; DNA; 84539 BP.
DE Osteoarthritis-associated polymorphic nucleotide #11.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.9%; Score 198.8; DB 10; Length 84539;
Best Local Similarity 75.6%; Pred. No. 7.5e-46;
RESULT 847
ID ADM29048 standard; DNA; 130020 BP.
DE Human interleukin 4 receptor (IL4R) genomic DNA SEQ ID NO:88.

PN EP1405921-A1.
PD 07-APR-2004.
PA (HOPE) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 21.9%; Score 198.8; DB 12; Length 130020;
Best Local Similarity 82.1%; Pred. No. 8.8e-46;
RESULT 848
ID ACN44070 standard; DNA; 344548 BP.
DE Human genomic sequence hCG35954.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 11; Length 344548;
Best Local Similarity 83.3%; Pred. No. 1.3e-45;
RESULT 849
ID ADQ97146 standard; DNA; 348101 BP.
DE Human cancer associated sequence HD08-007, SEQ ID 122.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.8; DB 12; Length 348101;
Best Local Similarity 82.1%; Pred. No. 1.3e-45;
RESULT 850
ID AAG62592 standard; cDNA; 1191 BP.
DE cDNA sequence #379 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 21.9%; Score 198.6; DB 6; Length 1191;
Best Local Similarity 85.4%; Pred. No. 1.7e-46;
RESULT 851
ID AAI58575 standard; cDNA; 1946 BP.
DE Human polynucleotide SEQ ID NO 778.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.6; DB 4; Length 1946;
Best Local Similarity 82.8%; Pred. No. 2e-46;
RESULT 852
ID ADQ98792 standard; cDNA; 1946 BP.
DE DNA encoding human GPCR-like protein seqid 462.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.6; DB 5; Length 1946;
Best Local Similarity 82.8%; Pred. No. 2e-46;
RESULT 853
ID ADB48552 standard; cDNA; 1946 BP.
DE Novel human cDNA SEQ ID NO 462.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 21.9%; Score 198.6; DB 9; Length 1946;
Best Local Similarity 82.8%; Pred. No. 2e-46;
RESULT 854
ID AAK83412 standard; DNA; 4156 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38224.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 4156;
Best Local Similarity 80.3%; Pred. No. 2.7e-46;
RESULT 855
ID AAK6667 standard; DNA; 4963 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23479.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 4963;

Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 856
ID AAT56538 standard; DNA; 4963 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2903.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 4963;
Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 857
ID ABX59526 standard; cDNA; 4963 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1870.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.9%; Score 198.6; DB 8; Length 4963;
Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 858
ID ADJ30276 standard; DNA; 4963 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2903.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 12; Length 4963;
Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 859
ID ADR06579 standard; cDNA; 5840 BP.
DE Full length human cDNA useful for treating neurological disease Seq 85.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.6; DB 13; Length 5840;
Best Local Similarity 82.8%; Pred. No. 3e-46;
RESULT 860
ID AAS26766 standard; DNA; 6096 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1740.
PN WO200153322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 6096;
Best Local Similarity 77.7%; Pred. No. 3.1e-46;
RESULT 861
ID ABX74115 standard; DNA; 6096 BP.
DE Human novel polynucleotide #943.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.9%; Score 198.6; DB 8; Length 6096;
Best Local Similarity 77.7%; Pred. No. 3.1e-46;
RESULT 862
ID ABK64514 standard; cDNA; 12263 BP.
DE Human cDNA differentially expressed in granulocytic cells #1085.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.9%; Score 198.6; DB 6; Length 12263;
Best Local Similarity 80.8%; Pred. No. 4.1e-46;
RESULT 863
ID ABA94501 standard; DNA; 15297 BP.
DE Human proto-oncogene tyrosine kinase genomic DNA sequence.
PN US6340584-B1.
PD 22-JAN-2002.
PA (PEKE-) PE CORP NY.
Query Match 21.9%; Score 198.6; DB 6; Length 15297;
Best Local Similarity 80.8%; Pred. No. 4.4e-46;
RESULT 864
ID ABV75414 standard; DNA; 15297 BP.
DE Human kinase genomic DNA sequence.
PN WO200277191-A2.

PD 03-OCT-2002.
PA (PEKE-) PE CORP NY.
Query Match 21.9%; Score 198.6; DB 8; Length 15297;
Best Local Similarity 80.8%; Pred. No. 4.4e-46;
RESULT 865
ID ADM28582 standard; cDNA; 15297 BP.
DE Human proto-oncogene tyrosine kinase DNA.
PN US2004063130-A1.
PD 01-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.6; DB 12; Length 15297;
Best Local Similarity 80.8%; Pred. No. 4.4e-46;
RESULT 866
ID AAK75677 standard; DNA; 16424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30489.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 16424;
Best Local Similarity 82.8%; Pred. No. 4.5e-46;
RESULT 867
ID AAK68448 standard; DNA; 16424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23260.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 16424;
Best Local Similarity 82.8%; Pred. No. 4.5e-46;
RESULT 868
ID ABA08132 standard; DNA; 32152 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 927.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 32152;
Best Local Similarity 74.8%; Pred. No. 5.9e-46;
RESULT 869
ID ADP75184 standard; DNA; 35192 BP.
DE Human ADAM19 gene fragment #4.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 21.9%; Score 198.6; DB 11; Length 35192;
Best Local Similarity 82.8%; Pred. No. 6.1e-46;
RESULT 870
ID ADQ97084 standard; DNA; 38690 BP.
DE Human cancer associated sequence HD10-004, SEQ ID 60.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.6; DB 12; Length 38690;
Best Local Similarity 82.8%; Pred. No. 6.3e-46;
RESULT 871
ID AAK78219 standard; DNA; 47090 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33031.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 47090;
Best Local Similarity 79.2%; Pred. No. 6.8e-46;
RESULT 872
ID AAK68725 standard; DNA; 47090 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23537.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 47090;
Best Local Similarity 79.2%; Pred. No. 6.8e-46;
RESULT 873
ID ABQ76896 standard; DNA; 53226 BP.
DE Human G-protein coupled receptor DNA SEQ ID 3.
PN US2002142951-A1.
PD 03-OCT-2002.

PA (WEBB/) WEBSTER M.
 PA (BEAS/) BEASLEY E. M.
 PA (KERC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 Query Match 21.9%; Score 198.6; DB 10; Length 53226;
 Best Local Similarity 82.8%; Pred. No. 7.1e-46;
 RESULT 874
 ID ADJ84182 standard; DNA; 76698 BP.
 DE Human c-raf genomic DNA which is a target for antisense therapy.
 PN WO2004003134-A2.
 PD 08-JUN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 76698;
 Best Local Similarity 82.8%; Pred. No. 8.2e-46;
 RESULT 875
 ID ABO88164 standard; cDNA; 86080 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 71.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (PROC-) PROCTER & GAMBLE CO.
 Query Match 21.9%; Score 198.6; DB 6; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 876
 ID ABR83561 standard; cDNA; 86080 BP.
 DE Human cDNA differentially expressed in granulocytic cells #132.
 PN WO20028999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 877
 ID ADD71054 standard; DNA; 86080 BP.
 DE Human protective protein for beta-galactosidase gene SEQ ID NO:58.
 PN WO2003061564-A2.
 PD 31-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (IGBI-) LG BIOMEDICAL INST.
 Query Match 21.9%; Score 198.6; DB 10; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 878
 ID ADQ18878 standard; DNA; 86080 BP.
 DE Human scot tissue sarcoma-upregulated DNA - SEQ ID 1697.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 86080;
 Best Local Similarity 82.7%; Pred. No. 8.6e-46;
 RESULT 879
 ID ADL13497 standard; DNA; 91823 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #29.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.9%; Score 198.6; DB 10; Length 91823;
 Best Local Similarity 82.7%; Pred. No. 8.8e-46;
 RESULT 880
 ID ACN444930 standard; DNA; 106378 BP.
 DE Human genomic sequence hCG1742422.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.6; DB 11; Length 106378;
 Best Local Similarity 80.3%; Pred. No. 9.3e-46;
 RESULT 881
 ID ADO32260 standard; DNA; 106707 BP.
 DE Human chromosome 20 region containing type 2 diabetes mellitus genes.
 PN WO2004039954-A2.
 PD 13-MAY-2004.
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 106707;
 Best Local Similarity 82.8%; Pred. No. 9.3e-46;
 RESULT 882

Query Match 21.9%; Score 198.6; DB 10; Length 110000;
 Best Local Similarity 84.1%; Pred. No. 9.4e-46;
 RESULT 883
 Query Match 21.9%; Score 198.6; DB 10; Length 110000;
 Best Local Similarity 84.1%; Pred. No. 9.4e-46;
 RESULT 884
 ID ABD32861 standard; DNA; 118466 BP.
 DE Human cancer-associated genomic DNA HD17-042.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.6; DB 13; Length 118466;
 Best Local Similarity 82.8%; Pred. No. 9.7e-46;
 RESULT 885
 ID ADQ97870 standard; DNA; 121160 BP.
 DE Human cancer associated sequence HD11-015. SEQ ID 847.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.6; DB 12; Length 121160;
 Best Local Similarity 84.3%; Pred. No. 9.8e-46;
 RESULT 886
 ID ABT10719 standard; cDNA; 122748 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 853.
 PN WO200259271-A2.
 PD 01-AUG-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 122748;
 Best Local Similarity 80.3%; Pred. No. 9.9e-46;
 RESULT 887
 ID ABL68213 standard; DNA; 145831 BP.
 DE Prostate cancer related gene sequence SEQ ID NO:7550.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 888
 ID ABL6806 standard; DNA; 145831 BP.
 DE Lung cancer related gene sequence SEQ ID NO:5143.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 889
 ID ABL68588 standard; DNA; 145831 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6925.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 890
 ID ABL62309 standard; DNA; 145831 BP.
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:646.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 891
 ID ABT10149 standard; cDNA; 145831 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 283.
 PN WO200259271-A2.
 PD 01-AUG-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.6; DB 6; Length 145831;
 Best Local Similarity 79.2%; Pred. No. 1.1e-45;
 RESULT 892
 ID AAH92378 standard; DNA; 700 BP.
 DE Human inflammatory bowel disease related gene fragment IGR1078a.
 PN WO200142511-A2.

PD 14-JUN-2001.
 PA (WHEP) WHITEHEAD INST BIOMEDICAL RES.
 DE (BLU1-) ELIPIPSIS BIOTHERAPEUTICS CORP.
 Query Match 21.9%; Score 198.4; DB 4; Length 700;
 Best Local Similarity 84.8%; Pred. No. 1.5e-46;
 RESULT 893
 ID ABK42296 standard; DNA; 1672 BP.
 DE Genomic sequence #195 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.4; DB 4; Length 1672;
 Best Local Similarity 81.0%; Pred. No. 2.2e-46;
 RESULT 894
 ID ADB60452 standard; DNA; 1672 BP.
 DE Connective tissue related genomic DNA #195.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.4; DB 9; Length 1672;
 Best Local Similarity 81.0%; Pred. No. 2.2e-46;
 RESULT 895
 ID ADM02728 standard; cDNA; 2549 BP.
 DE Human cDNA of the invention SEQ ID NO:1413.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY
 Query Match 21.9%; Score 198.4; DB 11; Length 2549;
 Best Local Similarity 78.8%; Pred. No. 2.5e-46;
 RESULT 896
 ID ABA21351 standard; DNA; 3843 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13682.
 PN WO200158063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.4; DB 5; Length 3843;
 Best Local Similarity 77.2%; Pred. No. 3e-46;
 RESULT 897
 ID AAT75298 standard; DNA; 7705 BP.
 DE Nucleotide sequence encoding human RAD50 3' end.
 PN WO9727284-A2.
 PD 31-JUL-1997.
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 Query Match 21.9%; Score 198.4; DB 2; Length 7705;
 Best Local Similarity 84.8%; Pred. No. 3.9e-46;
 RESULT 898
 ID ABK86218 standard; DNA; 13919 BP.
 DE DNA encoding AIP-1/FLASH promoter.
 PN WO200255691-A1.
 PD 18-JUL-2002.
 PA (NIRK-) NIRPON KAYAKU KK.
 Query Match 21.9%; Score 198.4; DB 6; Length 13919;
 Best Local Similarity 78.8%; Pred. No. 4.9e-46;
 RESULT 899
 ID ABK86221 standard; RNA; 13919 BP.
 DE AIP-1/FLASH promoter related RNA sequence.
 PN WO200255691-A1.
 PD 18-JUL-2002.
 PA (NIRK-) NIRPON KAYAKU KK.
 Query Match 21.9%; Score 198.4; DB 6; Length 13919;
 Best Local Similarity 78.8%; Pred. No. 4.9e-46;
 RESULT 900
 ID ABK86220 standard; DNA; 13919 BP.
 DE AIP-1/FLASH promoter related DNA sequence #2.
 PN WO200255691-A1.
 PD 18-JUL-2002.
 PA (NIRK-) NIRPON KAYAKU KK.
 Query Match 21.9%; Score 198.4; DB 6; Length 13919;
 Best Local Similarity 78.8%; Pred. No. 4.9e-46;
 RESULT 901
 ID ABK86229 standard; DNA; 21404 BP.
 DE AIP-1/FLASH promoter related DNA sequence #3.
 PN WO200255691-A1.

PD 18-JUL-2002.
 PA (NIRK-) NIRPON KAYAKU KK.
 Query Match 21.9%; Score 198.4; DB 6; Length 21404;
 Best Local Similarity 78.8%; Pred. No. 5.7e-46;
 RESULT 902
 ID ADR66994 standard; DNA; 22405 BP.
 DE Human cancer associated gene genomic sequence SEQ ID NO:40.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.4; DB 13; Length 22405;
 Best Local Similarity 82.2%; Pred. No. 5.8e-46;
 RESULT 903
 ID ADS36465 standard; DNA; 25322 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1679.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 21.9%; Score 198.4; DB 13; Length 25322;
 Best Local Similarity 78.8%; Pred. No. 6.1e-46;
 RESULT 904
 ID ADQ97189 standard; DNA; 29360 BP.
 DE Human cancer associated sequence HD08-012, SEQ ID 165.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.4; DB 12; Length 29360;
 Best Local Similarity 79.9%; Pred. No. 6.5e-46;
 RESULT 905
 ID AAK89230 standard; DNA; 30110 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 2806.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.4; DB 4; Length 30110;
 Best Local Similarity 78.4%; Pred. No. 6.5e-46;
 RESULT 906
 ID ADS36492 standard; DNA; 34059 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1706.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 21.9%; Score 198.4; DB 13; Length 34059;
 Best Local Similarity 78.8%; Pred. No. 6.9e-46;
 RESULT 907
 ID AAD31198 standard; DNA; 34634 BP.
 DE Human WKL-1 genomic DNA.
 PN EP1209229-A1.
 PD 29-MAY-2002.
 PA (LESC/) LESCH K.
 (MEYER/) MEYER J.
 Query Match 21.9%; Score 198.4; DB 6; Length 34634;
 Best Local Similarity 79.9%; Pred. No. 6.9e-46;
 RESULT 908
 ID ACN37238 standard; DNA; 48753 BP.
 DE Human periodontal disease related gene HSPG2 SEQ ID NO:148.
 PN WO2004042054-A1.
 PD 21-MAY-2004.
 PA (HUBI-) HUBIT GENOMIX INC.
 (KAMO/) KAMOI K.
 Query Match 21.9%; Score 198.4; DB 13; Length 48753;
 Best Local Similarity 84.8%; Pred. No. 7.9e-46;
 RESULT 909
 ID ACN45166 standard; DNA; 87687 BP.
 DE Human genomic sequence hCG31872.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.4; DB 11; Length 87687;
 Best Local Similarity 83.0%; Pred. No. 9.9e-46;
 RESULT 910
 ID ADP13458 standard; DNA; 87669 BP.
 DE Renal cell carcinoma differentially expressed gene #194.

PN W02004048933-A2.
 PD 10-JUN-2004.
 PA (AMWP) WYETH.
 PA (TWIN/) TWINE N C.
 PA (BUCR/) BURCZYNSKI M E.
 PA (TRBP/) TREPICCHIO W L.
 PA (DORN/) DORNER A.
 PA (STOV/) STOVER J A.
 PA (SLON/) SLONI D K.
 PA Query Match 21.9%; Score 198.4; DB 12; Length 87869;
 Best Local Similarity 82.6%; Pred. No. 9.9e-46;
 RESULT 911
 ID ACN45042 standard; DNA; 95835 BP.
 DE Human genomic sequence hCG37223.
 PN W02003073826-A2.
 PD 12-SEP-2003.
 PA (SAG-) SAGES DISCOVERY.
 PA Query Match 21.9%; Score 198.4; DB 11; Length 95835;
 Best Local Similarity 81.4%; Pred. No. 1e-45;
 RESULT 912
 ID ADE43582 standard; DNA; 128034 BP.
 DE Polymorphic human IDE genomic sequence, SEQ ID 187.
 PN W02003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 PA (GENH) GEN HOSPITAL CORP.
 PA Query Match 21.9%; Score 198.4; DB 10; Length 128034;
 Best Local Similarity 79.6%; Pred. No. 1.1e-45;
 RESULT 913
 ID ADH54060 standard; DNA; 128034 BP.
 DE Human IDE gene variant DNA sequence SegID187.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GENH) GEN HOSPITAL CORP.
 PA Query Match 21.9%; Score 198.4; DB 12; Length 128034;
 Best Local Similarity 79.6%; Pred. No. 1.1e-45;
 RESULT 914
 ID ABK8573 standard; cDNA; 130263 BP.
 DE Human cDNA differentially expressed in granulocytic cells #144.
 PN W0200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 PA Query Match 21.9%; Score 198.4; DB 6; Length 130263;
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 915
 ID AAL38336 standard; DNA; 143899 BP.
 DE Genomic sequence encoding a human NGR2 protein.
 PN W0200229059-A2.
 PD 11-APR-2002.
 PA (UYVA) UNIV VALE.
 PA (BIOJ) BIOGEN INC.
 PA Query Match 21.9%; Score 198.4; DB 6; Length 143899;
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 916
 ID ABL68122 standard; DNA; 174424 BP.
 DE Ovary cancer related gene sequence SEQ ID NO:6459.
 PN W0200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 PA Query Match 21.9%; Score 198.4; DB 6; Length 174424;
 Best Local Similarity 84.8%; Pred. No. 1.3e-45;
 RESULT 917
 ID ADQ19573 standard; DNA; 181343 BP.
 DE Human esot tissue sarcoma-upregulated DNA - SEQ ID 2392.
 PN W02004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PA Query Match 21.9%; Score 198.4; DB 12; Length 181343;
 Best Local Similarity 84.8%; Pred. No. 1.3e-45;
 RESULT 918
 ID ABX16034 standard; DNA; 203654 BP.
 DE Human gene encoding calcium channel transporter family member.
 PN US2002142938-A1.
 PD 03-OCT-2002.
 PA (YANC/) YAN C.
 PA (KETC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 PA Query Match 21.9%; Score 198.4; DB 10; Length 203654;
 Best Local Similarity 84.8%; Pred. No. 1.4e-45;
 RESULT 919
 ID ADL13471 standard; DNA; 214520 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #3.
 PN W02003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 PA Query Match 21.9%; Score 198.4; DB 10; Length 214520;
 Best Local Similarity 79.9%; Pred. No. 1.4e-45;
 RESULT 920
 ID AAV57926 standard; DNA; 235033 BP.
 DE Hereditary haemochromatosis subregion from an unaffected individual.
 PN W098144466-A1.
 PD 09-APR-1998.
 PA (PROG-) PROGENITOR INC.
 PA Query Match 21.9%; Score 198.4; DB 2; Length 235033;
 Best Local Similarity 82.2%; Pred. No. 1.4e-45;
 RESULT 921
 ID AAK6647 standard; DNA; 598 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21459.
 PN W0200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA Query Match 21.9%; Score 198.2; DB 4; Length 598;
 Best Local Similarity 81.7%; Pred. No. 1.7e-46;
 RESULT 922
 ID ADQ15750 standard; DNA; 1714 BP.
 DE 4 synthesis-period of neuroblastoma related DNA, SEQ ID 12.
 PN W02004039975-A1.
 PD 13-MAY-2004.
 PA (HISM) HISMITSU PHARM CO LTD.
 PA (CHIB-) CHIBA PREFECTURE.
 PA Query Match 21.9%; Score 198.2; DB 12; Length 1714;
 Best Local Similarity 80.5%; Pred. No. 2.5e-46;
 RESULT 923
 ID ADM02856 standard; cDNA; 2062 BP.
 DE Human cDNA of the trvention SEQ ID NO:1541.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA Query Match 21.9%; Score 198.2; DB 11; Length 2062;
 Best Local Similarity 72.7%; Pred. No. 2.7e-46;
 RESULT 924
 ID ABK34800 standard; cDNA; 2541 BP.
 DE Human cDNA for novel secreted protein, SEQ ID 569.
 PN W0200177290-A2.
 PD 18-OCT-2001.
 PA (GENV) GENETICS INST INC.
 PA Query Match 21.9%; Score 198.2; DB 6; Length 2541;
 Best Local Similarity 82.9%; Pred. No. 2.9e-46;
 RESULT 925
 ID ABK70289 standard; cDNA; 4824 BP.
 DE Human lung cancer associated full length cDNA DMSM-59.
 PN W0200224057-A2.
 PD 28-MAR-2002.
 PA (CORI-) CORIXA CORP.
 PA Query Match 21.9%; Score 198.2; DB 6; Length 4824;
 Best Local Similarity 72.7%; Pred. No. 3.7e-46;
 RESULT 926
 ID ADH28814 standard; DNA; 4824 BP.
 DE Human chronic myelogenous leukaemia (CML) gene marker #82.
 PN US2003104426-A1.
 PD 05-JUN-2003.
 PA (LINS/) LINSLEY P S.
 PA (MAOM/) MAO M.
 PA (DAIH/) DAI H.
 PA (HEIT/) HE Y.

PA (RAD1/) RAD1CH J P.
Query Match 21.9%; Score 198.2; DB 10; Length 4824;
Best Local Similarity 72.7%; Pred. No. 3.7e-46;
RESULT 927
ID ADR06591 standard; cDNA; 4865 BP.
DE Full length human cDNA useful for treating neurological disease Seq 97.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.2; DB 13; Length 4865;
Best Local Similarity 81.3%; Pred. No. 3.7e-46;
RESULT 928
ID AAS44656 standard; DNA; 4885 BP.
DE Human full-length polynucleotide sequence #81.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HISE-) HISEQ INC.
Query Match 21.9%; Score 198.2; DB 4; Length 4885;
Best Local Similarity 72.7%; Pred. No. 3.7e-46;
RESULT 929
ID AAK60970 standard; DNA; 6159 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35782.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.2; DB 4; Length 6159;
Best Local Similarity 80.8%; Pred. No. 4.1e-46;
RESULT 930
ID AAD32327 standard; DNA; 15765 BP.
DE Human NFKB1B gene, alternative version.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 21.9%; Score 198.2; DB 6; Length 15765;
Best Local Similarity 79.2%; Pred. No. 5.8e-46;
RESULT 931
ID AAD32179 standard; DNA; 15765 BP.
DE Human NFKB1B gene.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 21.9%; Score 198.2; DB 6; Length 15765;
Best Local Similarity 79.2%; Pred. No. 5.8e-46;
RESULT 932
ID AAK74096 standard; DNA; 21777 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28908.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.2; DB 4; Length 21777;
Best Local Similarity 80.5%; Pred. No. 6.6e-46;
RESULT 933
ID AAS17764 standard; DNA; 24843 BP.
DE Human genomic DNA for CRYBL.
PN WO200185998-A1.
PD 15-NOV-2001.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 21.9%; Score 198.2; DB 6; Length 24843;
Best Local Similarity 81.7%; Pred. No. 6.9e-46;
RESULT 934
ID ADR67086 standard; DNA; 29328 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:132.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.2; DB 13; Length 29328;
Best Local Similarity 77.4%; Pred. No. 7.4e-46;
RESULT 935
ID AAL04340 standard; DNA; 32194 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7028.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 21.9%; Score 198.2; DB 4; Length 32194;
Best Local Similarity 82.9%; Pred. No. 7.7e-46;
RESULT 936
ID ADS19371 standard; DNA; 37940 BP.
DE Human PIP5K type II beta related DNA #1.
PN US2003232777-A1.
PD 18-DEC-2003.
PA (MARC-) MARCUSON B G.
PA (DORI/) DORIE K W.
PA (FREI/) FREIER S M.
Query Match 21.9%; Score 198.2; DB 13; Length 37940;
Best Local Similarity 75.9%; Pred. No. 8.2e-46;
RESULT 937
ID ADJ26093 standard; DNA; 38000 BP.
DE Human PIP5KII-beta genomic DNA SeqID 11.
PN US2003232775-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.9%; Score 198.2; DB 12; Length 38000;
Best Local Similarity 75.9%; Pred. No. 8.2e-46;
RESULT 938
ID ACN45050 standard; DNA; 41966 BP.
DE Human genomic sequence hCG39344.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.2; DB 11; Length 41966;
Best Local Similarity 80.5%; Pred. No. 8.5e-46;
RESULT 939
ID ADB16927 standard; DNA; 49806 BP.
DE Human DYX1C DNA, chromosomal gene region nucleotides 50001-100000.
PN WO2003068814-A1.
PD 21-AUG-2003.
PA (LICN) LICENTIA LTD.
Query Match 21.9%; Score 198.2; DB 9; Length 49806;
Best Local Similarity 82.7%; Pred. No. 9.1e-46;
RESULT 940
ID ABD32754 standard; DNA; 62124 BP.
DE Human cancer-associated genomic DNA HD16-028.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.2; DB 13; Length 62124;
Best Local Similarity 82.9%; Pred. No. 9.9e-46;
RESULT 941
ID ADO25290 standard; DNA; 80928 BP.
DE Human protein kinase C iota/lambda genomic sequence.
PN WO2004041212-A2.
PD 21-MAY-2004.
PA (SACK/) SACKTOR T C.
PA (CRAR/) CRARY J F.
PA (HERN/) HERNANDEZ A I.
PA (MIRR/) MIRRA S.
PA (SHAO/) SHAO C.
Query Match 21.9%; Score 198.2; DB 12; Length 80928;
Best Local Similarity 79.4%; Pred. No. 1.1e-45;
RESULT 942
ID AAF64800 standard; DNA; 110000 BP.
DE Nucleotide sequence of the human SPG4 gene.
PN FR2798138-A1.
PD 09-MAR-2001.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 21.9%; Score 198.2; DB 5; Length 110000;
Best Local Similarity 80.5%; Pred. No. 1.2e-45;
RESULT 943
Query Match 21.9%; Score 198.2; DB 6; Length 110000;
Best Local Similarity 82.9%; Pred. No. 1.2e-45;
RESULT 944
ID AC013448 standard; DNA; 115756 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 68.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Query Match 21.9%; Score 198.2; DB 8; Length 115756;
 Best Local Similarity 85.6%; Pred. No. 1.3e-45;
 RESULT 945
 ID ADJ79662 standard; DNA; 123526 BP.
 DE Human glioma-associated oncogene-3 related DNA, SEQ ID NO 11.
 PN WO2003008549-A2.
 PD 30-JAN-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.9%; Score 198.2; DB 10; Length 123526;
 Best Local Similarity 81.9%; Pred. No. 1.3e-45;
 RESULT 946
 ID AAV57903 standard; DNA; 237326 BP.
 DE Hereditary haemochromatosis subregion from an HH affected individual.
 PN WO9814466-A1.
 PD 09-APR-1998.
 PA (PROG-) PROCENTOR INC.
 Query Match 21.9%; Score 198.2; DB 2; Length 237326;
 Best Local Similarity 82.9%; Pred. No. 1.7e-45;
 RESULT 947
 ID ADQ59422 standard; DNA; 246940 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
 PN WO2004058288-A1.
 PD 15-UTL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.9%; Score 198.2; DB 12; Length 246940;
 Best Local Similarity 78.9%; Pred. No. 1.7e-45;
 RESULT 948
 ID ADC87010 standard; DNA; 349999 BP.
 DE Human GPCR gene SEQ ID NO:11463.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 21.9%; Score 198.2; DB 10; Length 349999;
 Best Local Similarity 75.5%; Pred. No. 1.9e-45;
 RESULT 949
 ID ADQ24208 standard; DNA; 1911 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7028.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 1911;
 Best Local Similarity 78.0%; Pred. No. 3e-46;
 RESULT 950
 ID ADM01910 standard; cDNA; 2460 BP.
 DE Human cDNA of the invention SEQ ID NO:595.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.8%; Score 198; DB 11; Length 2460;
 Best Local Similarity 81.6%; Pred. No. 3.3e-46;
 RESULT 951
 ID AAK69971 standard; DNA; 7770 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23783.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 7770;
 Best Local Similarity 83.6%; Pred. No. 5.1e-46;
 RESULT 952
 ID AAK76477 standard; DNA; 9409 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31289.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 9409;
 Best Local Similarity 81.2%; Pred. No. 5.5e-46;
 RESULT 953
 ID AAD34213 standard; DNA; 9432 BP.
 DE Human cytochrome P450 2D6 (CYP2D6) gene.
 PN WO200218638-A2.
 PD 07-MAR-2002.
 PA (GEMI-) GEMINI GENOMICS PLC.

Query Match 21.8%; Score 198; DB 6; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 954
 ID ACA61301 standard; DNA; 9432 BP.
 DE Human cytochrome P450 gene CYP2D6, wild-type.
 PN EP1281755-A2.
 PD 05-FEB-2003.
 PA (PFIZ) PFIZER PROD INC.
 Query Match 21.8%; Score 198; DB 10; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 955
 ID ADF83400 standard; DNA; 9432 BP.
 DE Human CYP2D6 gene (wild-type).
 PN WO2003100091-A1.
 PD 04-DEC-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 956
 ID ADJ78563 standard; DNA; 9432 BP.
 DE Human cytochrome P450 isoenzyme 2D6 genomic gene sequence SeqID1.
 PN WO2004009760-A2.
 PD 29-JAN-2004.
 PA (BIOV-) BIOVENTURES INC.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 957
 ID ADM28891 standard; DNA; 9432 BP.
 DE Human wild-type CYP2D6 gene sequence.
 PN US2004072235-A1.
 PD 15-APR-2004.
 PA (DAMS/) DAWSON E P.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 958
 ID ACA61302 standard; DNA; 9433 BP.
 DE Human cytochrome P450 gene CYP2D6, variant sequence.
 PN EP1281755-A2.
 PD 05-FEB-2003.
 PA (PFIZ) PFIZER PROD INC.
 Query Match 21.8%; Score 198; DB 10; Length 9433;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 959
 ID AAL06376 standard; DNA; 11557 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9064.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 960
 ID AAL06375 standard; DNA; 11557 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9063.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 961
 ID AAS32244 standard; DNA; 11557 BP.
 DE Human DNA repair and processing genomic DNA #30.
 PN WO200155204-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 5; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 962
 ID AAS32243 standard; DNA; 11557 BP.
 DE Human DNA repair and processing genomic DNA #29.
 PN WO200155204-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 5; Length 11557;

Best Local Similarity 82.6%; Pred. No. 5.9e-46;
RESULT 963
ID ABS67547 standard; DNA; 11557 BP.
DE Novel human DNA repair protein, genomic sequence #30.
PN US2002086353-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.8%; Score 198; DB 6; Length 11557;
Best Local Similarity 82.6%; Pred. No. 5.9e-46;
RESULT 964
ID ABS67546 standard; DNA; 11557 BP.
DE Novel human DNA repair protein, genomic sequence #29.
PN US2002086353-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.8%; Score 198; DB 6; Length 11557;
Best Local Similarity 82.6%; Pred. No. 5.9e-46;
RESULT 965
ID AAK79132 standard; DNA; 14379 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33944.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 14379;
Best Local Similarity 83.8%; Pred. No. 6.4e-46;
RESULT 966
ID AAS26724 standard; DNA; 19472 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1698.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 19472;
Best Local Similarity 75.1%; Pred. No. 7.2e-46;
RESULT 967
ID ABX74073 standard; DNA; 19472 BP.
DE Human novel polynucleotide #901.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.8%; Score 198; DB 8; Length 19472;
Best Local Similarity 75.1%; Pred. No. 7.2e-46;
RESULT 968
ID AAL03615 standard; DNA; 32134 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6303.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32134;
Best Local Similarity 82.4%; Pred. No. 8.7e-46;
RESULT 969
ID ABA07813 standard; DNA; 32134 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 608.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32134;
Best Local Similarity 82.4%; Pred. No. 8.7e-46;
RESULT 970
ID AAL03616 standard; DNA; 32191 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6304.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32191;
Best Local Similarity 82.4%; Pred. No. 8.8e-46;
RESULT 971
ID ABA07814 standard; DNA; 32191 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 609.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32191;
Best Local Similarity 82.4%; Pred. No. 8.8e-46;
RESULT 972
ID ABA20618 standard; DNA; 32220 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12949.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 5; Length 32220;
Best Local Similarity 80.1%; Pred. No. 8.8e-46;
RESULT 973
ID ABX61804 standard; DNA; 40645 BP.
DE Genomic DNA encoding novel human GABA transporter related protein.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY B M.
Query Match 21.8%; Score 198; DB 8; Length 40645;
Best Local Similarity 76.7%; Pred. No. 9.6e-46;
RESULT 974
ID ADA49717 standard; DNA; 40645 BP.
DE Genomic DNA encoding human transporter protein.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY B M.
Query Match 21.8%; Score 198; DB 8; Length 40645;
Best Local Similarity 76.7%; Pred. No. 9.6e-46;
RESULT 975
ID AAK71437 standard; DNA; 52845 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26249.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 52845;
Best Local Similarity 83.5%; Pred. No. 1.1e-45;
RESULT 976
ID ACM44918 standard; DNA; 55114 BP.
DE Human genomic sequence hCG20493.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 11; Length 55114;
Best Local Similarity 82.4%; Pred. No. 1.1e-45;
RESULT 977
ID ADA02684 standard; DNA; 59817 BP.
DE Human DUSP10 carcinoma associated gene, SEQ ID NO:1202.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 9; Length 59817;
Best Local Similarity 82.6%; Pred. No. 1.1e-45;
RESULT 978
ID ADB72422 standard; DNA; 59817 BP.
DE Human DUSP10 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 10; Length 59817;
Best Local Similarity 82.6%; Pred. No. 1.1e-45;
RESULT 979
ID ADB55932 standard; DNA; 59817 BP.
DE Human DUSP10 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 10; Length 59817;
Best Local Similarity 82.6%; Pred. No. 1.1e-45;
RESULT 980
ID ADA42934 standard; DNA; 70000 BP.
DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.

PN US6410325-B1.
 PD 25-JUN-2002.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 198; DB 6; Length 70000;
 Best Local Similarity 80.1%; Pred. No. 1.2e-45;
 RESULT 981
 ID ACN44938 standard; DNA; 73771 BP.
 DE Human genomic sequence hCG37394.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 11; Length 73771;
 Best Local Similarity 82.8%; Pred. No. 1.2e-45;
 RESULT 982
 ID AAL57572 standard; cDNA; 107818 BP.
 DE Human phosphomannomutase 1 cDNA.
 PN WO2003059148-A2.
 PD 24-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 198; DB 9; Length 107818;
 Best Local Similarity 80.8%; Pred. No. 1.4e-45;
 RESULT 983
 Query Match 21.8%; Score 198; DB 10; Length 110000;
 Best Local Similarity 75.1%; Pred. No. 1.4e-45;
 RESULT 984
 Query Match 21.8%; Score 198; DB 10; Length 110000;
 Best Local Similarity 75.1%; Pred. No. 1.4e-45;
 RESULT 985
 ID ADQ19183 standard; DNA; 110665 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2002.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 110665;
 Best Local Similarity 76.0%; Pred. No. 1.4e-45;
 RESULT 986
 ID ADQ17641 standard; DNA; 114771 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 458.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 114771;
 Best Local Similarity 78.8%; Pred. No. 1.4e-45;
 RESULT 987
 ID ADQ97319 standard; DNA; 117829 BP.
 DE Human cancer associated sequence HD08-031, SEQ ID 296.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.8%; Score 198; DB 12; Length 117829;
 Best Local Similarity 76.0%; Pred. No. 1.4e-45;
 RESULT 988
 ID ADH63063 standard; DNA; 132762 BP.
 DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
 PN WO2003024987-A1.
 PD 27-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 198; DB 10; Length 132762;
 Best Local Similarity 82.6%; Pred. No. 1.5e-45;
 RESULT 989
 ID AAK8497 standard; cDNA; 149671 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1368.
 PN WO200228899-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 198; DB 6; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 990
 ID ADB70361 standard; cDNA; 149671 BP.
 DE Moesin cDNA SEQ ID NO:53.
 PN WO2003021229-A2.
 PD 13-MAR-2003.

PA (BGM-) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 21.8%; Score 198; DB 9; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 991
 ID ADJ37140 standard; cDNA; 149671 BP.
 DE Human malignant pleural mesothelioma. (MPM) cDNA #23.
 PN US2003219760-A1.
 PD 27-NOV-2003.
 PA (BGM-) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 21.8%; Score 198; DB 12; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 992
 ID ADL13752 standard; DNA; 190000 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #284.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.8%; Score 198; DB 10; Length 190000;
 Best Local Similarity 81.2%; Pred. No. 1.7e-45;
 RESULT 993
 ID ADF14037 standard; DNA; 1167 BP.
 DE Human endometrial-specific DNA - SEQ ID 2.
 PN WO2003059927-A1.
 PD 24-JUL-2003.
 PA (DIND-) DINDEXUS INC.
 Query Match 21.8%; Score 197.8; DB 10; Length 1167;
 Best Local Similarity 75.7%; Pred. No. 2.8e-46;
 RESULT 994
 ID AAC69633 standard; cDNA; 1295 BP.
 DE Human secreted protein gene 37 SEQ ID NO:47.
 PN WO200056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 3; Length 1295;
 Best Local Similarity 77.5%; Pred. No. 2.9e-46;
 RESULT 995
 ID AAK35888 standard; cDNA; 3705 BP.
 DE cDNA sequence #279 encoding novel human secreted protein.
 PN WO200177289-A2.
 PD 18-OCT-2001.
 PA (GENY-) GENETICS INST INC.
 Query Match 21.8%; Score 197.8; DB 6; Length 3705;
 Best Local Similarity 78.0%; Pred. No. 4.3e-46;
 RESULT 996
 ID AAI57935 standard; cDNA; 6610 BP.
 DE Human polynucleotide SEQ ID NO 138.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 6610;
 Best Local Similarity 82.1%; Pred. No. 5.4e-46;
 RESULT 997
 ID AAK51636 standard; cDNA; 7005 BP.
 DE Human polynucleotide SEQ ID NO 181.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 7005;
 Best Local Similarity 82.1%; Pred. No. 5.6e-46;
 RESULT 998
 ID AAK38061 standard; DNA; 16707 BP.
 DE Genomic DNA for Human GABAB receptors.
 PN WO9921890-A1.
 PD 06-MAY-1999.
 PA (ASTR-) ASTRA AB.
 Query Match 21.8%; Score 197.8; DB 2; Length 16707;
 Best Local Similarity 80.7%; Pred. No. 7.8e-46;
 RESULT 999
 ID AAI03177 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6065.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;
 RESULT 1000
 ID AAL03378 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6066.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;
 RESULT 1001
 ID AAL03379 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6067.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 21913;
 Best Local Similarity 77.9%; Pred. No. 8.6e-46;
 RESULT 1002
 ID AAK70624 standard; DNA; 24768 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25436.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 24768;
 Best Local Similarity 80.5%; Pred. No. 9e-46;
 RESULT 1003
 ID AD181379 standard; DNA; 25001 BP.
 DE Human P2X4 genomic DNA sequence.
 PN US2004002152-A1.
 PD 01-JAN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 197.8; DB 13; Length 25001;
 Best Local Similarity 76.9%; Pred. No. 9.1e-46;
 RESULT 1004
 ID ADH36221 standard; DNA; 28616 BP.
 DE Human purinergic receptor P2X4 gene sequence.
 PN WO2003101177-A2.
 PD 11-DEC-2003.
 PA (SEQU-) SEQUENOM INC.
 Query Match 21.8%; Score 197.8; DB 12; Length 28616;
 Best Local Similarity 76.9%; Pred. No. 9.6e-46;
 RESULT 1005
 ID AAS32492 standard; DNA; 32191 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 446.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 32191;
 Best Local Similarity 77.5%; Pred. No. 1e-45;
 RESULT 1006
 ID ACN44490 standard; DNA; 32865 BP.
 DE Human genomic sequence hCG25375.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.8; DB 11; Length 32865;
 Best Local Similarity 78.5%; Pred. No. 1e-45;
 RESULT 1007
 ID AAK71918 standard; DNA; 42048 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26730.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 42048;
 Best Local Similarity 79.6%; Pred. No. 1.1e-45;
 RESULT 1008
 ID AAG46140 standard; DNA; 50000 BP.
 DE Nucleotide sequence of a beta-tubulin antigen.
 PN WO200050593-A1.
 PD 31-AUG-2000.
 PA (UYTE-) UNIV TENNESSEE RES CORP.
 Query Match 21.8%; Score 197.8; DB 3; Length 50000;

Best Local Similarity 81.7%; Pred. No. 1.2e-45;
 RESULT 1009
 ID AAD30228 standard; DNA; 53522 BP.
 DE Human PKD1 gene.
 PN WO200206529-A2.
 PD 24-JAN-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Query Match 21.8%; Score 197.8; DB 6; Length 53522;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;
 RESULT 1010
 ID AAT94101 standard; DNA; 53526 BP.
 DE Human PKD1 gene.
 PN WO9744457-A1.
 PD 27-NOV-1997.
 PA (GENZ-) GENZYME CORP.
 Query Match 21.8%; Score 197.8; DB 2; Length 53526;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;
 RESULT 1011
 ID AAT18551 standard; DNA; 53577 BP.
 DE Human polycystic kidney disease normal PKD1 gene.
 PN WO9612033-A1.
 PD 25-APR-1996.
 PA (IGIG-) IG LAB INC.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 21.8%; Score 197.8; DB 2; Length 53577;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;
 RESULT 1012
 ID AAT94108 standard; DNA; 53577 BP.
 DE Human PKD1 locus between chromosomal markers ATP6 (ATP6C) and D16S84.
 PN WO9744457-A1.
 PD 27-NOV-1997.
 PA (GENZ-) GENZYME CORP.
 Query Match 21.8%; Score 197.8; DB 2; Length 53577;
 Best Local Similarity 80.5%; Pred. No. 1.2e-45;
 RESULT 1013
 ID AAK83212 standard; DNA; 68356 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 68356;
 Best Local Similarity 80.5%; Pred. No. 1.3e-45;
 RESULT 1014
 ID AAK67283 standard; DNA; 68356 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 68356;
 Best Local Similarity 80.5%; Pred. No. 1.3e-45;
 RESULT 1015
 ID ACN44710 standard; DNA; 70242 BP.
 DE Human genomic sequence hCG1784894.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.8; DB 11; Length 70242;
 Best Local Similarity 80.7%; Pred. No. 1.3e-45;
 RESULT 1016
 ID ADP53001 standard; DNA; 96256 BP.
 DE Drug therapy altered expressed gene #352.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP-) WYETH.
 PA (BURC-) BURCZYNSKI M.
 PA (TWIN-) TWINE N.
 PA (DORN-) DORNER A J.
 PA (TREP-) TREPCICHO W L.
 Query Match 21.8%; Score 197.8; DB 13; Length 96256;
 Best Local Similarity 80.7%; Pred. No. 1.5e-45;
 RESULT 1017
 ID ABR12169 standard; DNA; 98690 BP.
 DE Human DNA representing the Tachykinin Receptor 1, TACR1, gene.

PN WO200216399-A2.
 PD 28-FEB-2002.
 PA (GENA-) GENAISSANCE PHARM INC.
 Query Match 21.8%; Score 197.8; DB 6; Length 98690;
 Best Local Similarity 84.5%; Pred. No. 1.5e-45;
 RESULT 1018
 ID ABT44365 standard; DNA; 113000 BP.
 DE Partial genomic sequence of human oestrogen receptor beta DNA.
 PN WO2003050133-A1.
 PD 19-JUN-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 197.8; DB 9; Length 113000;
 Best Local Similarity 84.5%; Pred. No. 1.6e-45;
 RESULT 1019
 ID ADE43581 standard; DNA; 128034 BP.
 DE Human IDE genomic sequence, SEQ ID 186.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 PA (GENO-) GEN HOSPITAL CORP.
 Query Match 21.8%; Score 197.8; DB 10; Length 128034;
 Best Local Similarity 79.6%; Pred. No. 1.7e-45;
 RESULT 1020
 ID ADH54059 standard; DNA; 128034 BP.
 DE Human IDE gene DNA sequence SeqID186.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GENO-) GEN HOSPITAL CORP.
 Query Match 21.8%; Score 197.8; DB 12; Length 128034;
 Best Local Similarity 79.6%; Pred. No. 1.7e-45;
 RESULT 1021
 ID ACN44074 standard; DNA; 128668 BP.
 DE Human genomic sequence hCG40471.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGES DISCOVERY.
 Query Match 21.8%; Score 197.8; DB 11; Length 128668;
 Best Local Similarity 80.7%; Pred. No. 1.7e-45;
 RESULT 1022
 ID ACA64895 standard; DNA; 134292 BP.
 DE Human GABBR1 DNA corresponding to AL031983.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATH-) PATHOARRAY GMBH.
 Query Match 21.8%; Score 197.8; DB 8; Length 134292;
 Best Local Similarity 80.7%; Pred. No. 1.7e-45;
 RESULT 1023
 ID ABK83562 standard; cDNA; 139904 BP.
 DE Human cDNA differentially expressed in granulocytic cells #133.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 197.8; DB 6; Length 139904;
 Best Local Similarity 81.7%; Pred. No. 1.8e-45;
 RESULT 1024
 ID AAZ86667 standard; DNA; 162450 BP.
 DE Retinoblastoma binding protein-7 genomic DNA sequence.
 PN WO20000607-A1.
 PD 06-JAN-2000.
 PA (GEST-) GEST.
 Query Match 21.8%; Score 197.8; DB 3; Length 162450;
 Best Local Similarity 80.7%; Pred. No. 1.9e-45;
 RESULT 1025
 ID ADE43315 standard; DNA; 202100 BP.
 DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 PA (GENO-) GEN HOSPITAL CORP.
 Query Match 21.8%; Score 197.8; DB 10; Length 202100;
 Best Local Similarity 79.6%; Pred. No. 2e-45;
 RESULT 1026
 ID ADH54357 standard; DNA; 202100 BP.

DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GENO-) GEN HOSPITAL CORP.
 Query Match 21.8%; Score 197.8; DB 12; Length 202100;
 Best Local Similarity 79.6%; Pred. No. 2e-45;
 RESULT 1027
 ID ADE86352 standard; DNA; 300000 BP.
 DE Human PTPN11 genomic DNA sequence SEQ ID NO:33.
 PN WO2003029422-A2.
 PD 10-APR-2003.
 PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
 Query Match 21.8%; Score 197.8; DB 10; Length 300000;
 Best Local Similarity 82.3%; Pred. No. 2.4e-45;
 RESULT 1028
 ID ADO14076 standard; DNA; 300001 BP.
 DE Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33.
 PN WO2004041216-A2.
 PD 21-MAY-2004.
 PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
 PA (UNIV-) UNIVERSITÄTSKLINIKUM FREIBURG.
 Query Match 21.8%; Score 197.8; DB 12; Length 300001;
 Best Local Similarity 82.3%; Pred. No. 2.4e-45;
 RESULT 1029
 ID AAS43104 standard; DNA; 325791 BP.
 DE Human Oestrogen receptor beta gene.
 PN WO200162793-A2.
 PD 30-AUG-2001.
 PA (PEKE-) PE CORP NY.
 Query Match 21.8%; Score 197.8; DB 4; Length 325791;
 Best Local Similarity 84.5%; Pred. No. 2.4e-45;
 RESULT 1030
 ID ABX61844 standard; DNA; 601 BP.
 DE Novel human transporter protein related polynucleotide #40.
 PN US2002142381-A1.
 PD 03-OCT-2002.
 PA (GONG/) GONG F.
 PA (KERC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 21.8%; Score 197.6; DB 8; Length 601;
 Best Local Similarity 76.4%; Pred. No. 2.5e-46;
 RESULT 1031
 ID ABX61842 standard; DNA; 601 BP.
 DE Novel human transporter protein related polynucleotide #38.
 PN US2002142381-A1.
 PD 03-OCT-2002.
 PA (GONG/) GONG F.
 PA (KERC/) KETCHUM K A.
 PA (DFRA/) DI FRANCESCO V.
 PA (BEAS/) BEASLEY E M.
 Query Match 21.8%; Score 197.6; DB 8; Length 601;
 Best Local Similarity 76.4%; Pred. No. 2.5e-46;
 RESULT 1032
 ID ADF30333 standard; cDNA; 993 BP.
 DE Human cancer suppressing protein pP12616-encoding cDNA, SEQ:25 and 27.
 PN CN1368508-A.
 PD 11-SEP-2002.
 PA (SHAN-) SHANGHAI INST ONCOLOGY.
 Query Match 21.8%; Score 197.6; DB 10; Length 993;
 Best Local Similarity 77.0%; Pred. No. 3e-46;
 RESULT 1033
 ID AAH14398 standard; cDNA; 2182 BP.
 DE Human cDNA sequence SEQ ID NO:11832.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 21.8%; Score 197.6; DB 4; Length 2182;
 Best Local Similarity 84.3%; Pred. No. 4e-46;
 RESULT 1034
 ID ABK35751 standard; cDNA; 2702 BP.
 DE cDNA sequence #142 encoding novel human secreted protein.
 PN WO200177289-A2.

PD 18-OCT-2001.
PA (GENV) GENETICS INST INC.
Query Match 21.8%; Score 197.6; DB 6; Length 2702;
Best Local Similarity 84.3%; Pred. No. 4.4e-46;
RESULT 1035
ID ABV75593 standard; DNA; 3509 BP.
DE Novel human gene #6.
PN WO200277257-A1.
PD 03-OCT-2002.
PA (HISE-) HISEQ INC.
Query Match 21.8%; Score 197.6; DB 10; Length 3509;
Best Local Similarity 84.3%; Pred. No. 4.9e-46;
RESULT 1036
ID AAK3053 standard; DNA; 5331 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37865.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 5331;
Best Local Similarity 80.5%; Pred. No. 5.7e-46;
RESULT 1037
ID AAK3051 standard; DNA; 7022 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37863.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 7022;
Best Local Similarity 80.5%; Pred. No. 6.3e-46;
RESULT 1038
ID AAK3820 standard; DNA; 11840 BP.
DE Humane immune/haematopoietic antigen genomic sequence SEQ ID NO:38632.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 11840;
Best Local Similarity 76.4%; Pred. No. 7.8e-46;
RESULT 1039
ID AAS28506 standard; DNA; 23626 BP.
DE Genomic sequence #346 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1040
ID ABA21480 standard; DNA; 23626 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13811.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1041
ID AAS2997 standard; DNA; 23626 BP.
DE Human lung antigen genomic DNA #67.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1042
ID ADB33334 standard; DNA; 23626 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 261.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1043
ID ADG41702 standard; DNA; 23626 BP.
DE Human respiratory system associated genomic DNA seq id 940.
PN US2003215893-A1.
PD 20-NOV-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1044
ID ADI97476 standard; DNA; 23626 BP.
DE Human respiratory system associated polypeptide-related DNA seqID940.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 11; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1045
ID AAS28507 standard; DNA; 23632 BP.
DE Genomic sequence #347 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1046
ID ABA21481 standard; DNA; 23632 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13812.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1047
ID AAS29998 standard; DNA; 23632 BP.
DE Human lung antigen genomic DNA #68.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1048
ID ADB33335 standard; DNA; 23632 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 262.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1049
ID ADG41703 standard; DNA; 23632 BP.
DE Human respiratory system associated genomic DNA seq id 941.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1050
ID ADI97477 standard; DNA; 23632 BP.
DE Human respiratory system associated polypeptide-related DNA seqID941.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 11; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1051
ID ADL27170 standard; DNA; 29040 BP.
DE Human genomic sequence for LFNG.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 21.8%; Score 197.6; DB 11; Length 29040;
Best Local Similarity 84.3%; Pred. No. 1.1e-45;
RESULT 1052
ID ADA03092 standard; DNA; 29322 BP.
DE Human LFNG carcinoma associated gene. SEQ ID NO:1610.
PN WO2003057146-A2.
PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.6; DB 9; Length 29322;
 Best Local Similarity 84.3%; Pred. No. 1.1e-45;
 RESULT 1053
 ID ADA66376 standard; DNA; 29322 BP.
 DE Human LTRNG gene genomic DNA sequence.
 PN WO2003053224-A2.
 PD 03-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.6; DB 9; Length 29322;
 Best Local Similarity 84.3%; Pred. No. 1.1e-45;
 RESULT 1054
 ID ADB72830 standard; DNA; 29322 BP.
 DE Human LTRNG gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.6; DB 10; Length 29322;
 Best Local Similarity 84.3%; Pred. No. 1.1e-45;
 RESULT 1055
 ID AAK68677 standard; DNA; 34269 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23489.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.6; DB 4; Length 34269;
 Best Local Similarity 74.4%; Pred. No. 1.2e-45;
 RESULT 1056
 ID AAK85168 standard; DNA; 34269 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39980.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.6; DB 4; Length 34269;
 Best Local Similarity 74.4%; Pred. No. 1.2e-45;
 RESULT 1057
 ID ADS86040 standard; DNA; 37797 BP.
 DE Tumour treatment-related human gene sequence SegID76.
 PN WO2004034995-A2.
 PD 29-APR-2004.
 PA (UYPT-) UNIV PITTSBURGH.
 Query Match 21.8%; Score 197.6; DB 13; Length 37797;
 Best Local Similarity 80.3%; Pred. No. 1.2e-45;
 RESULT 1058
 ID ACN44534 standard; DNA; 39768 BP.
 DE Human genomic sequence hCG38101.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.6; DB 11; Length 39768;
 Best Local Similarity 78.1%; Pred. No. 1.2e-45;
 RESULT 1059
 ID ABD33318 standard; DNA; 52987 BP.
 DE Human cancer-associated (CA) gene HD07-057.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.8%; Score 197.6; DB 13; Length 52987;
 Best Local Similarity 77.1%; Pred. No. 1.4e-45;
 RESULT 1060
 ID ACC45150 standard; DNA; 96649 BP.
 DE Human NAC nucleotide sequence SEQ ID NO:10.
 PN WO2003024988-A1.
 PD 27-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 197.6; DB 8; Length 96649;
 Best Local Similarity 80.3%; Pred. No. 1.7e-45;
 RESULT 1061
 ID ACB36634 standard; cDNA; 463 BP.
 DE Human endothelial cell cDNA #4767.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 Query Match 21.8%; Score 197.6; DB 12; Length 110000;
 Best Local Similarity 73.6%; Pred. No. 1.8e-45;
 RESULT 1062
 ID ACH36634 standard; cDNA; 463 BP.
 DE Human endothelial cell cDNA #4767.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 Query Match 21.8%; Score 197.6; DB 12; Length 110000;
 Best Local Similarity 73.6%; Pred. No. 1.8e-45;

RESULT 1063
 ID ACA64961 standard; DNA; 152141 BP.
 DE Human BCR DNA corresponding to U07000.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATH-) PATHOARRAY GMBH.
 Query Match 21.8%; Score 197.6; DB 8; Length 152141;
 Best Local Similarity 84.0%; Pred. No. 2.1e-45;
 RESULT 1064
 ID ABK83571 standard; cDNA; 175737 BP.
 DE Human cDNA differentially expressed in granulocytic cells #142.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 197.6; DB 6; Length 175737;
 Best Local Similarity 76.8%; Pred. No. 2.2e-45;
 RESULT 1065
 ID ADL13596 standard; DNA; 175737 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #128.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.8%; Score 197.6; DB 10; Length 175737;
 Best Local Similarity 76.6%; Pred. No. 2.2e-45;
 RESULT 1066
 ID ADQ18934 standard; DNA; 175737 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1753.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 197.6; DB 12; Length 175737;
 Best Local Similarity 76.6%; Pred. No. 2.2e-45;
 RESULT 1067
 ID ACN44010 standard; DNA; 198522 BP.
 DE Human genomic sequence hCG1643869.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 197.6; DB 11; Length 198522;
 Best Local Similarity 78.7%; Pred. No. 2.3e-45;
 RESULT 1068
 ID ABS56564 standard; DNA; 260209 BP.
 DE Human SUF2 genomic DNA sequence.
 PN WO200259327-A2.
 PD 01-AUG-2002.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 21.8%; Score 197.6; DB 6; Length 260209;
 Best Local Similarity 86.9%; Pred. No. 2.6e-45;
 RESULT 1069
 ID ADN16204 standard; DNA; 260209 BP.
 DE Human sulfatase SUF1 gene.
 PN WO2004031365-A2.
 PD 15-APR-2004.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 21.8%; Score 197.6; DB 12; Length 260209;
 Best Local Similarity 86.9%; Pred. No. 2.6e-45;
 RESULT 1070
 ID ABK89296 standard; DNA; 326014 BP.
 DE Human gene for novel serine/threonine kinase.
 PN WO2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 Query Match 21.8%; Score 197.6; DB 12; Length 326014;
 Best Local Similarity 80.3%; Pred. No. 2.8e-45;
 RESULT 1071
 ID ADQ94981 standard; DNA; 326014 BP.
 DE Human kinase genomic DNA.
 PN WO2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 Query Match 21.8%; Score 197.6; DB 12; Length 326014;
 Best Local Similarity 80.3%; Pred. No. 2.8e-45;
 RESULT 1072
 ID ACH36634 standard; cDNA; 463 BP.
 DE Human endothelial cell cDNA #4767.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 Query Match 21.8%; Score 197.6; DB 12; Length 326014;
 Best Local Similarity 80.3%; Pred. No. 2.8e-45;

PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 9; Length 463;
RESULT 1073
ID ADB83200 standard; cDNA; 588 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 1413).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 9; Length 588;
RESULT 1074
ID AAH98452 standard; cDNA; 874 BP.
DE Human EST-derived coding sequence SEQ ID NO: 309.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 4; Length 874;
RESULT 1075
ID ADG10849 standard; cDNA; 1539 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:439.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 10; Length 1599;
RESULT 1076
ID AAK75888 standard; DNA; 3891 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:30700.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 4; Length 3891;
RESULT 1077
ID AAK90709 standard; DNA; 5032 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4285.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 4; Length 5032;
RESULT 1078
ID ABD33436 standard; DNA; 52710 BP.
DE Human cancer-associated (CA) gene HD07-082.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 13; Length 52710;
RESULT 1079
ID ABD33470 standard; DNA; 61765 BP.
DE Human cancer-associated (CA) gene HD07-090.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 13; Length 61765;
RESULT 1080
ID ACN44362 standard; DNA; 68255 BP.
DE Human genomic sequence hCG39597.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 11; Length 68255;
RESULT 1081
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 6; Length 110000;

Best Local Similarity 84.8%; Pred. No. 2.1e-45;
RESULT 1082
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 6; Length 110000;
RESULT 1083
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 8; Length 110000;
RESULT 1084
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 12; Length 110000;
RESULT 1085
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 12; Length 110000;
RESULT 1086
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 13; Length 110000;
RESULT 1087
ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVML-) AVMLON PHARM.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 6; Length 174424;
RESULT 1088
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 12; Length 181343;
RESULT 1089
ID AAT62346 standard; DNA; 282 BP.
DE Consensus Alu repeat sequence.
PN US5597694-A.
PD 28-JAN-1997.
PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 2; Length 282;
RESULT 1090
ID AAF22565 standard; cDNA; 537 BP.
DE Human breast cancer associated antigen nucleotide sequence SEQ ID NO:144.
PN WO200073801-A2.
PD 07-DEC-2000.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 4; Length 537;
RESULT 1091
ID ABN61073 standard; cDNA; 662 BP.
DE Human cancer related polynucleotide SEQ ID NO 1040.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 6; Length 662;
RESULT 1092
ID ACC86725 standard; DNA; 751 BP.
DE Human VEGFR-1 nucleotide sequence SEQ ID NO:20.
PN WO2003022237-A2.
PD 20-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 8; Length 751;
RESULT 1093
ID AAH16580 standard; cDNA; 2092 BP.
DE Human cDNA sequence SEQ ID NO:15661.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 4; Length 2092;

RESULT 1094
ID ADF81697 standard; DNA; 4908 BP.
DE Leukemia-related DNA sequence #2253.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFB/) HAFERLACH T.
PA (SCHC/) SCHUCH C.
PA (KERN/) KERN W.
Query Match 21.7%; Score 197.2; DB 10; Length 4908;
Best Local Similarity 72.4%; Pred. No. 7.2e-46;
RESULT 1095
ID ADF81698 standard; DNA; 4908 BP.
DE Leukemia-related DNA sequence #2254.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFB/) HAFERLACH T.
PA (SCHC/) SCHUCH C.
PA (KERN/) KERN W.
Query Match 21.7%; Score 197.2; DB 10; Length 4908;
Best Local Similarity 72.4%; Pred. No. 7.2e-46;
RESULT 1096
ID AAK73007 standard; DNA; 6658 BP.
DE Human immune/haematopoietic antigen genomic*sequence SEQ ID NO:27819.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 6658;
Best Local Similarity 83.3%; Pred. No. 8.1e-46;
RESULT 1097
ID AAL03021 standard; DNA; 6658 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5709.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 6658;
Best Local Similarity 83.3%; Pred. No. 8.1e-46;
RESULT 1098
ID AAL06167 standard; DNA; 8577 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8855.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 8577;
Best Local Similarity 81.8%; Pred. No. 8.9e-46;
RESULT 1099
ID ABL98732 standard; DNA; 8577 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3384.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 8577;
Best Local Similarity 81.8%; Pred. No. 8.9e-46;
RESULT 1100
ID ABA17047 standard; DNA; 8577 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9378.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 5; Length 8577;
Best Local Similarity 81.8%; Pred. No. 8.9e-46;
RESULT 1101
ID AAK8986 standard; DNA; 32224 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3562.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 32224;
Best Local Similarity 84.2%; Pred. No. 1.5e-45;
RESULT 1102

ID ABD33190 standard; DNA; 33478 BP.
DE Human cancer-associated (CA) gene HD07-028.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.7%; Score 197.2; DB 13; Length 33478;
Best Local Similarity 84.2%; Pred. No. 1.5e-45;
RESULT 1103
ID ABN96830 standard; DNA; 40433 BP.
DE Gene #3328 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.7%; Score 197.2; DB 6; Length 40433;
Best Local Similarity 80.5%; Pred. No. 1.6e-45;
RESULT 1104
ID ADA02528 standard; DNA; 57763 BP.
DE Human MYB carcinoma associated gene, SEQ ID NO:1046.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 197.2; DB 9; Length 57763;
Best Local Similarity 80.5%; Pred. No. 1.9e-45;
RESULT 1105
ID ADB72266 standard; DNA; 57763 BP.
DE Human MYB gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 197.2; DB 10; Length 57763;
Best Local Similarity 80.5%; Pred. No. 1.9e-45;
RESULT 1106
ID ADE95776 standard; DNA; 57763 BP.
DE Human MYB gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 197.2; DB 10; Length 57763;
Best Local Similarity 80.5%; Pred. No. 1.9e-45;
RESULT 1107
ID ADJ53477 standard; DNA; 70000 BP.
DE Human PPP3CB genomic DNA #3.
PN US2004023382-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.7%; Score 197.2; DB 12; Length 70000;
Best Local Similarity 85.8%; Pred. No. 2e-45;
RESULT 1108
ID AAK85590 standard; DNA; 75384 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40402.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 75384;
Best Local Similarity 80.3%; Pred. No. 2.1e-45;
RESULT 1109
ID ADJ33364 standard; DNA; 92139 BP.
DE 92kb gene fragment in human chromosome 17 at 17q21.
PN WO200210455-A2.
PD 07-FEB-2002.
PA (CELU-) CELLTECH R & D INC.
PA (STRA/) STRAHLING HAMPTON K.
Query Match 21.7%; Score 197.2; DB 6; Length 92139;
Best Local Similarity 80.5%; Pred. No. 2.2e-45;
RESULT 1110
ID AAD53324 standard; DNA; 567571 BP.
DE Human chromosome 3 q-arm breakpoint region.
PN WO200290541-A1.
PD 14-NOV-2002.
PA (MURD-) MURDOCH CHILDRENS RES INST.
PA (DELA/) DELATYCKI M.
Query Match 21.7%; Score 197.2; DB 8; Length 110000;
Best Local Similarity 84.5%; Pred. No. 2.4e-45;

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RESULT 1111
Query Match      21.7%; Score 197.2; DB 11; Length 110000;
Best Local Similarity 78.9%; Pred. No. 2.4e-45;
RESULT 1112
Query Match      21.7%; Score 197.2; DB 11; Length 110000;
Best Local Similarity 78.9%; Pred. No. 2.4e-45;
RESULT 1113
Query Match      21.7%; Score 197.2; DB 11; Length 110000;
Best Local Similarity 74.0%; Pred. No. 2.4e-45;
RESULT 1114
ID ADH76849 standard; DNA; 122557 BP.
DE Melanin-concentrating hormone receptor 1 locus clone.
PN WO2003104489-A2.
PD 18-DEC-2003.
PA (UYRH-) UNIV PHILIPPS MARBURG.
Query Match      21.7%; Score 197.2; DB 12; Length 122557;
Best Local Similarity 78.6%; Pred. No. 2.5e-45;
RESULT 1115
ID ADO80254 standard; cDNA; 127145 BP.
DE Hermansky-Pudlak syndrome associated cDNA.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match      21.7%; Score 197.2; DB 13; Length 127145;
Best Local Similarity 74.6%; Pred. No. 2.5e-45;
RESULT 1116
ID ADP11613 standard; DNA; 130320 BP.
DE Human sclerostin gene region.
PN WO2003087763-A2.
PD 23-OCT-2003.
PA (CELL-) CELLTECH R & D INC.
DE (UYRO-) UNIV ROTTERDAM ERASMUS.
Query Match      21.7%; Score 197.2; DB 10; Length 130320;
Best Local Similarity 80.5%; Pred. No. 2.5e-45;
RESULT 1117
ID ADQ97183 standard; DNA; 138627 BP.
DE Human cancer associated sequence HD08-011, SEQ ID 159.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      21.7%; Score 197.2; DB 13; Length 138627;
Best Local Similarity 84.5%; Pred. No. 2.6e-45;
RESULT 1118
ID AA195194 standard; cDNA; 717 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1269.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
DE (HISM-) HISAMITSU PHARM CO LTD.
Query Match      21.7%; Score 197; DB 4; Length 717;
Best Local Similarity 75.1%; Pred. No. 3.9e-46;
RESULT 1119
ID AAS32730 standard; DNA; 1515 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 684.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 1515;
Best Local Similarity 82.4%; Pred. No. 5.2e-46;
RESULT 1120
ID ABL55355 standard; cDNA; 2408 BP.
DE Human protein synthesis initiation factor 10.12-encoding cDNA.
PN CN1331221-A.
PD 16-JAN-2002.
PA (BOBE-) BOBE GENE DEV CO LTD SHANGHAI.
Query Match      21.7%; Score 197; DB 6; Length 2408;
Best Local Similarity 80.0%; Pred. No. 6.3e-46;
RESULT 1121
ID ACC50229 standard; cDNA; 2969 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:301.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match      21.7%; Score 197; DB 13; Length 2969;
Best Local Similarity 82.5%; Pred. No. 6.8e-46;
RESULT 1122
ID ADR07810 standard; cDNA; 3779 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1316.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      21.7%; Score 197; DB 13; Length 3779;
Best Local Similarity 83.7%; Pred. No. 7.4e-46;
RESULT 1123
ID ADR08449 standard; cDNA; 3834 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1955.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      21.7%; Score 197; DB 13; Length 3834;
Best Local Similarity 78.9%; Pred. No. 7.5e-46;
RESULT 1124
ID ADR07292 standard; cDNA; 3868 BP.
DE Full length human cDNA useful for treating neurological disease Seq 798.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      21.7%; Score 197; DB 13; Length 3868;
Best Local Similarity 78.9%; Pred. No. 7.5e-46;
RESULT 1125
ID AAK85025 standard; DNA; 5919 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39837.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 5919;
Best Local Similarity 79.2%; Pred. No. 8.8e-46;
RESULT 1126
ID AAZ59353 standard; DNA; 8396 BP.
DE Human SRP2 (phenol sulphotransferase 2) gene.
PN WO9964630-A1.
PD 16-DEC-1999.
PA (AXYS-) AXYS PHARM INC.
Query Match      21.7%; Score 197; DB 3; Length 8396;
Best Local Similarity 74.2%; Pred. No. 1e-45;
RESULT 1127
ID AAK89550 standard; DNA; 13246 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3126.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 13246;
Best Local Similarity 82.5%; Pred. No. 1.2e-45;
RESULT 1128
ID AAK89551 standard; DNA; 13247 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3127.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 13247;
Best Local Similarity 82.5%; Pred. No. 1.2e-45;
RESULT 1129
ID ABD32570 standard; DNA; 22047 BP.
DE Human cancer-associated genomic DNA HD7-165.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      21.7%; Score 197; DB 13; Length 22047;
Best Local Similarity 77.9%; Pred. No. 1.5e-45;
RESULT 1130
ID ABD33137 standard; DNA; 22056 BP.
DE Human cancer-associated (CA) gene HD07-016.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      21.7%; Score 197; DB 13; Length 22056;
```

Best Local Similarity 77.9%; Pred. No. 1.5e-45;
 RESULT 1131
 ID AAK61639 standard; DNA; 28011 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:36451.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 28011;
 Best Local Similarity 82.4%; Pred. No. 1.6e-45;
 RESULT 1132
 ID ADC67584 standard; DNA; 28066 BP.
 DE Human GPCR gene SEQ ID NO:2037.
 PN EPI270724-A2.
 PD 02-JAN-2003.
 PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 DE (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 21.7%; Score 197; DB 10; Length 28066;
 Best Local Similarity 77.9%; Pred. No. 1.6e-45;
 RESULT 1133
 ID AAK90296 standard; DNA; 32199 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3872.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1134
 ID AAI57673 standard; DNA; 32199 BP.
 DE Human colorectal cancer antigen coding sequence SEQ ID NO: 210.
 PN WO200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1135
 ID ABS9850 standard; DNA; 32199 BP.
 DE Genomic DNA #54 encoding human colorectal cancer related protein.
 PN US2002119919-A1.
 PD 29-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BAR/) BARASH S C.
 Query Match 21.7%; Score 197; DB 6; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1136
 ID ADB93003 standard; DNA; 32199 BP.
 DE Human colorectal cancer related polypeptide DNA #54.
 PN US2003054420-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 10; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1137
 ID ADQ59482 standard; DNA; 43709 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:118.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 197; DB 12; Length 43709;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1138
 ID ACN45130 standard; DNA; 61197 BP.
 DE Human genomic sequence hCG15017.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 61197;
 Best Local Similarity 77.3%; Pred. No. 2.2e-45;
 RESULT 1139
 ID ACN44082 standard; DNA; 71048 BP.
 DE Human genomic sequence hCG39199.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 71048;
 Best Local Similarity 83.7%; Pred. No. 2.3e-45;
 RESULT 1140
 ID ACN44422 standard; DNA; 114931 BP.
 DE Human genomic sequence hCG27894.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 114931;
 Best Local Similarity 80.0%; Pred. No. 2.8e-45;
 RESULT 1141
 ID AAV52850 standard; DNA; 116624 BP.
 DE Human eyal gene contig 4405-9480.
 PN WO9832849-A2.
 PD 30-JUL-1998.
 PA (INSP-) INST PASTEUR.
 Query Match 21.7%; Score 197; DB 2; Length 116624;
 Best Local Similarity 80.0%; Pred. No. 2.8e-45;
 RESULT 1143
 ID ACN44574 standard; DNA; 116792 BP.
 DE Human genomic sequence hCG18576.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 116792;
 Best Local Similarity 79.2%; Pred. No. 2.8e-45;
 RESULT 1144
 ID ADI29095 standard; DNA; 119501 BP.
 DE Human MARK3 genomic DNA.
 PN US2003232771-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 197; DB 12; Length 119501;
 Best Local Similarity 79.8%; Pred. No. 2.8e-45;
 RESULT 1145
 ID ADH50806 standard; DNA; 119596 BP.
 DE Human G-protein coupled receptor gene.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Query Match 21.7%; Score 197; DB 6; Length 119596;
 Best Local Similarity 77.3%; Pred. No. 2.8e-45;
 RESULT 1146
 ID ADE43582 standard; DNA; 128034 BP.
 DE Polymorphic human IDB genomic sequence, SEQ ID 187.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Query Match 21.7%; Score 197; DB 10; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1147
 ID ADE43581 standard; DNA; 128034 BP.
 DE Human IDB genomic sequence, SEQ ID 186.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Query Match 21.7%; Score 197; DB 10; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1148
 ID ADH54059 standard; DNA; 128034 BP.
 DE Human IDB gene DNA sequence SeqID186.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 21.7%; Score 197; DB 12; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1149
 ID ADH54060 standard; DNA; 128034 BP.
 DE Human IDB gene variant DNA sequence SeqID187.
 PN US2003224380-A1.

PD 04-DEC-2003.
PA (GENO) GEN HOSPITAL CORP.
Query Match 21.7%; Score 197; DB 12; Length 128034;
Best Local Similarity 80.0%; Pred. No. 2.9e-45;
RESULT 1150
ID ABRN65735 standard; DNA; 155074 BP.
DE Human genomic region containing the ltrp5 gene SEQ ID NO 6.
PN WO200254069-A1.
PD 11-JUL-2002.
PA (RESC) UNIV CALIFORNIA.
Query Match 21.7%; Score 197; DB 6; Length 155074;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1151
ID ADQ040461 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 197; DB 12; Length 166181;
Best Local Similarity 82.5%; Pred. No. 3.2e-45;
RESULT 1152
ID ADQ18633 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 197; DB 12; Length 166181;
Best Local Similarity 82.5%; Pred. No. 3.2e-45;
RESULT 1153
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.7%; Score 197; DB 11; Length 174448;
Best Local Similarity 78.9%; Pred. No. 3.3e-45;
RESULT 1154
ID ADL13935 standard; DNA; 177866 BP.
DE Osteoarthritis-associated polymorphic nucleotide #467.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.7%; Score 197; DB 10; Length 177866;
Best Local Similarity 84.0%; Pred. No. 3.3e-45;
RESULT 1155
ID ACN44598 standard; DNA; 212231 BP.
DE Human genomic sequence hCG401221.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.7%; Score 197; DB 11; Length 212231;
Best Local Similarity 77.1%; Pred. No. 3.5e-45;
RESULT 1156
ID ACN44194 standard; DNA; 275449 BP.
DE Human genomic sequence hCG23995.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.7%; Score 197; DB 11; Length 275449;
Best Local Similarity 80.0%; Pred. No. 3.9e-45;
RESULT 1157
ID ADB62528 standard; cDNA; 2308 BP.
DE Human cDNA encoding clone HNDPC20082790.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 21.7%; Score 196.8; DB 10; Length 2308;
Best Local Similarity 78.5%; Pred. No. 7e-46;
RESULT 1158
ID ADQ66839 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3714.
PN WO2004060270-A2.

PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 12; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1159
ID ADQ83620 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #434.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1160
ID ADQ84294 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1108.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1161
ID ADQ84044 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #858.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1162
ID ACN40563 standard; cDNA; 2320 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA236655, SEQ ID NO:5419.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1163
ID ADM02495 standard; cDNA; 2404 BP.
DE Human cDNA of the invention SEQ ID NO:1180.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.7%; Score 196.8; DB 11; Length 2404;
Best Local Similarity 78.5%; Pred. No. 7.1e-46;
RESULT 1164
ID ABO83600 standard; cDNA; 2631 BP.
DE Human fumarate reductase/succinic dehydrogenase 9.13 cDNA SEQ ID NO:1.
PN CN1345948-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 21.7%; Score 196.8; DB 6; Length 2631;
Best Local Similarity 84.7%; Pred. No. 7.4e-46;
RESULT 1165
ID AAK66744 standard; DNA; 5079 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21556.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 5079;
Best Local Similarity 79.5%; Pred. No. 9.5e-46;
RESULT 1166
ID ADQ24919 standard; DNA; 6833 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7739.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 196.8; DB 12; Length 6833;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1167
ID ADQ24145 standard; DNA; 6833 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6965.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 196.8; DB 12; Length 6833;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1168
ID AAI62666 standard; DNA; 7444 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 316.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1169
ID AAI6760 standard; DNA; 7444 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9448.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1170
ID AAI66118 standard; DNA; 7444 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8806.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1171
ID AAI96683 standard; DNA; 7444 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3335.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1172
ID ABA15867 standard; DNA; 7444 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8198.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 5; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1173
ID AAK66749 standard; DNA; 9324 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21561.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9324;
Best Local Similarity 79.5%; Pred. No. 1.2e-45;
RESULT 1174
ID AAS28695 standard; DNA; 9765 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 257.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1175
ID AAS28886 standard; DNA; 9755 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 248.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1176
ID ABA15616 standard; DNA; 15187 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7947.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1177
ID ABA06802 standard; DNA; 9765 BP.
DE Human genomic DNA SEQ ID NO: 888.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1178
ID ABA06849 standard; DNA; 9765 BP.
DE Human genomic DNA SEQ ID NO: 935.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1179
ID ABA064139 standard; DNA; 9765 BP.
DE Human polynucleotide SEQ ID NO 888.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBS/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.7%; Score 196.8; DB 6; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1180
ID ABA064139 standard; DNA; 9765 BP.
DE Human polynucleotide SEQ ID NO 935.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBS/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.7%; Score 196.8; DB 6; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1181
ID ABA15616 standard; DNA; 15187 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7947.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 15186;
Best Local Similarity 82.0%; Pred. No. 1.5e-45;
RESULT 1182
ID AAS42100 standard; DNA; 12595 BP.
DE Genomic sequence #416 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 10; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1183
ID ABA15617 standard; DNA; 15186 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7948.
PN WO2001559063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 5; Length 15186;
Best Local Similarity 82.0%; Pred. No. 1.5e-45;
RESULT 1184
ID ABA15616 standard; DNA; 15187 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7947.

PN WO00159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 5; Length 15187;
 Best Local Similarity 82.0%; Pred. No. 1.5e-45;
 RESULT 1185
 ID AAK66680 standard; DNA; 17357 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41492.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 17357;
 Best Local Similarity 83.2%; Pred. No. 1.5e-45;
 RESULT 1186
 ID AAK66681 standard; DNA; 17363 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41493.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 17363;
 Best Local Similarity 83.2%; Pred. No. 1.5e-45;
 RESULT 1187
 ID ADC66168 standard; DNA; 21704 BP.
 DE Human GPCR gene SEQ ID NO:621.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (MAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 21.7%; Score 196.8; DB 10; Length 21704;
 Best Local Similarity 79.5%; Pred. No. 1.7e-45;
 RESULT 1188
 ID ADQ97776 standard; DNA; 25694 BP.
 DE Human cancer associated sequence HD10-045, SEQ ID 753.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 25694;
 Best Local Similarity 78.5%; Pred. No. 1.8e-45;
 RESULT 1189
 ID ABS52813 standard; DNA; 27847 BP.
 DE Genomic DNA encoding human secreted protein #1.
 PN WO200264626-A2.
 PD 22-AUG-2002.
 PA (PEKE-) PE CORP NY.
 Query Match 21.7%; Score 196.8; DB 6; Length 27847;
 Best Local Similarity 81.8%; Pred. No. 1.8e-45;
 RESULT 1190
 ID ADQ97189 standard; DNA; 29360 BP.
 DE Human cancer associated sequence HD08-012, SEQ ID 165.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 29360;
 Best Local Similarity 80.7%; Pred. No. 1.9e-45;
 RESULT 1191
 ID AAJ37292 standard; DNA; 32192 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3657.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 32192;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1192
 ID AAL07103 standard; DNA; 32192 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9791.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 32192;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1193
 ID ABX60280 standard; cDNA; 32192 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2624.

PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 21.7%; Score 196.8; DB 8; Length 32192;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1194
 ID ADJ31030 standard; DNA; 32192 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3657.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 32192;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1195
 ID AB64428 standard; DNA; 35641 BP.
 DE Stomach cancer related gene sequence SEQ ID NO:2765.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.7%; Score 196.8; DB 6; Length 35641;
 Best Local Similarity 82.0%; Pred. No. 2e-45;
 RESULT 1196
 ID ABN95727 standard; DNA; 35641 BP.
 DE Gene #2925 used to diagnose liver cancer.
 PN WO200228103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.7%; Score 196.8; DB 6; Length 35641;
 Best Local Similarity 82.0%; Pred. No. 2e-45;
 RESULT 1197
 ID AAK72372 standard; DNA; 37925 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27184.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 37925;
 Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 RESULT 1198
 ID ADJ12847 standard; DNA; 37925 BP.
 DE DNA fragment of a BAC clone that encodes a human secreted protein Seq701.
 PN US2004010132-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (BREM/) BREWER L A.
 PA (DUAN/) DUAN R D.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (GRE/) GREENE J M.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRIE A M.
 PA (YUG/) YU G.
 PA (FLOR/) FLORENCE C.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match 21.7%; Score 196.8; DB 12; Length 37925;
 Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 RESULT 1199
 ID ABX65018 standard; DNA; 43545 BP.
 DE Human cadherin-like asymmetry protein-2 (CLASP-2) genomic DNA.
 PN WO200231117-A2.
 PD 18-APR-2002.
 PA (ARBO-) ARBOR VITA CORP.
 PA (GARM/) GARMAN J D.
 PA (CAND/) CANDIA A F.
 Query Match 21.7%; Score 196.8; DB 6; Length 43545;
 Best Local Similarity 76.9%; Pred. No. 2.2e-45;
 RESULT 1200
 ID ADA02960 standard; DNA; 44325 BP.
 DE Human DAD1 carcinoma associated gene, SEQ ID NO:1478.
 PN WO2003057146-A2.
 PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.8; DB 9; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1201
 ID ADB72698 standard; DNA; 44325 BP.
 DE Human DAD1 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.8; DB 10; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1202
 ID ADC85440 standard; DNA; 44325 BP.
 DE Human Dad1 genomic sequence.
 PN WO2003045230-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.8; DB 10; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1203
 ID ADM74555 standard; DNA; 44325 BP.
 DE Human carcinoma associated (CA) nucleic acid #112.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR/) MORRIS D W.
 PA (ENGEL/) ENGELHARD E K.
 Query Match 21.7%; Score 196.8; DB 12; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1204
 ID ABD32574 standard; DNA; 45944 BP.
 DE Human cancer-associated genomic DNA HD7-204.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 45944;
 Best Local Similarity 81.8%; Pred. No. 2.2e-45;
 RESULT 1205
 ID ADA42934 standard; DNA; 70000 BP.
 DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.
 PN US6410323-B1.
 PD 25-JUN-2002.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.8; DB 6; Length 70000;
 Best Local Similarity 79.5%; Pred. No. 2.6e-45;
 RESULT 1206
 Query Match 21.7%; Score 196.8; DB 12; Length 87411;
 Best Local Similarity 79.1%; Pred. No. 2.8e-45;
 RESULT 1207
 ID ABD33432 standard; DNA; 106938 BP.
 DE Human cancer-associated (CA) gene HD07-081.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 106938;
 Best Local Similarity 81.8%; Pred. No. 3.1e-45;
 RESULT 1208
 ID ADR67034 standard; DNA; 106938 BP.
 DE Human cancer associated gene genomic sequence SEQ ID NO:80.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 106938;
 Best Local Similarity 81.8%; Pred. No. 3.1e-45;
 RESULT 1209
 ID ADL17884 standard; cDNA; 158001 BP.
 DE Human phosphotyrosyl phosphatase activator, PTPA, gene.
 PN US2004023906-A1.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 158001;
 Best Local Similarity 84.5%; Pred. No. 3.6e-45;
 RESULT 1210
 ID ACA64924 standard; DNA; 201239 BP.

DE Human PLZF DNA corresponding to AF060568.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATR-) PATHOARRAY GMBH.
 Query Match 21.7%; Score 196.8; DB 8; Length 201239;
 Best Local Similarity 80.7%; Pred. No. 3.9e-45;
 RESULT 1211
 ID AAA69691 standard; cDNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:1.
 PN WO2000036107-A2.
 PD 22-JUN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 3; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1212
 ID AAA69693 standard; cDNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:3.
 PN WO2000036107-A2.
 PD 22-JUN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 3; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1213
 ID ABR72587 standard; DNA; 461 BP.
 DE Ovarian carcinoma antigen polynucleotide #3.
 PN WO200206317-A2.
 PD 24-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 6; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1214
 ID ABR72585 standard; DNA; 461 BP.
 DE Ovarian carcinoma antigen polynucleotide #1.
 PN WO200206317-A2.
 PD 24-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 6; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1215
 ID ADA08752 standard; DNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide #3.
 PN US2003091580-A1.
 PD 15-MAY-2003.
 PA (MITC/) MITCHAM J L.
 PA (KING/) KING G E.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 PA (REED/) REED S G.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 Query Match 21.7%; Score 196.6; DB 9; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1216
 ID ADA08750 standard; DNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide #1.
 PN US2003091580-A1.
 PD 15-MAY-2003.
 PA (MITC/) MITCHAM J L.
 PA (KING/) KING G E.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 PA (REED/) REED S G.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 Query Match 21.7%; Score 196.6; DB 9; Length 461;

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Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1217
ID ADP08499 standard; cDNA; 461 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 3.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1218
ID ADP08497 standard; cDNA; 461 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 1.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1219
ID ADG46247 standard; cDNA; 461 BP.
DE Human ovarian carcinoma polynucleotide #3.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1220
ID ADG46245 standard; cDNA; 461 BP.
DE Human ovarian carcinoma polynucleotide #1.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1221
ID AAH15355 standard; cDNA; 1652 BP.
DE Human cDNA sequence SEQ ID NO:13531.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 21.7%; Score 196.6; DB 4; Length 1652;
Best Local Similarity 80.2%; Pred. No. 7.1e-46;
RESULT 1222
ID AAS21268 standard; cDNA; 3719 BP.
DE Human cDNA sequence encoding for PRO4799 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 4; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1223
ID ACA03627 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1224
ID ABX69165 standard; cDNA; 3719 BP.
DE DNA encoding novel secreted and transmembrane protein PRO4799.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1225
ID ACD1819 standard; cDNA; 3719 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #25.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1226
ID ACA04046 standard; cDNA; 3719 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 49.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1227
ID ADA45568 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1228
ID ADA75999 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1229
ID ADA18649 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1230
ID ADA61272 standard; cDNA; 3719 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1231
ID ADB19057 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1232
ID ADB27598 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1233
ID ADA86077 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1234
ID ADB15641 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
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ID ADA74895 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1254
ID ADA84973 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1255
ID ADA84421 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1256
ID ADB29677 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1257
ID ADA80205 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1258
ID ADA75447 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1259
ID ADA46672 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1260
ID ADB24968 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1261
ID ADA93144 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1262
ID ADB26494 standard; cDNA; 3719 BP.

DE cDNA encoding human PRO polypeptide #25.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1263
ID ADB30781 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1264
ID ADA60709 standard; cDNA; 3719 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1265
ID ADB23856 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1266
ID ADA96185 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1267
ID ADA80757 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1268
ID ADA95633 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1269
ID ADB25942 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1270
ID ADB21427 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1271
ID ADA77206 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.

PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1272
ID ADB17946 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1273
ID ADA86629 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1274
ID ADA87732 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1275
ID ADA46120 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1276
ID ADB28150 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1277
ID ADB28702 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1278
ID ADA76654 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1279
ID ADA88284 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1280
ID ADA937289 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082686-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1281
ID ADB27046 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1282
ID ADB21979 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1283
ID ADA66670 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1284
ID ADB22531 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1285
ID ADB23304 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1286
ID ADA92026 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1287
ID ADB15089 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1288
ID ADB38341 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1289
ID ADB37789 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;

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Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1290
ID ADB86261 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1291
ID ADB89341 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1292
ID ADB80073 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1293
ID ADB39174 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1294
ID ADB86797 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1295
ID ADB86404 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082657-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1296
ID ADB77009 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082656-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1297
ID ADB34166 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1298
ID ADB35270 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1299
ID ADB33614 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1300
ID ADB34718 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1301
ID ADB35822 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1302
ID ADB46217 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1303
ID ADC50090 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1304
ID ADC71637 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1305
ID ADC59616 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1306
ID ADC52623 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID49.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1307
ID ADC56977 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID49.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1308
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ID ADCC60168 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087367-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1309
 ID ADC50643 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087361-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1310
 ID ADC65170 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003087362-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1311
 ID ADC54268 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087363-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1312
 ID ADC53329 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087364-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1313
 ID ADC58752 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087359-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1314
 ID ADC55630 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087360-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1315
 ID ADC58200 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087346-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1316
 ID ADD02874 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092104-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1317
 ID ADC89866 standard; cDNA; 3719 BP.

DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087348-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1318
 ID ADC69285 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1319
 ID ADC48174 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194773-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1320
 ID ADD09703 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194776-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1321
 ID ADD04278 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087354-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1322
 ID ADC80234 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092103-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1323
 ID ADD10741 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1324
 ID ADC47622 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1325
 ID ADC79682 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087358-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1326
 ID ADD09151 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.

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PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1327
ID ADD40864 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1328
ID ADD52003 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1329
ID ADD52743 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1330
ID ADD53295 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1331
ID ADD51451 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1332
ID ADD02250 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1333
ID ADD01684 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1334
ID ADD35866 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1335
ID ADD92183 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199030-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1336
ID ADD91079 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1337
ID ADE03693 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1338
ID ADE31990 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1339
ID ADE21922 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1340
ID ADD79146 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1341
ID ADE41682 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1342
ID ADE17499 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1343
ID ADD91631 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1344
ID ADE33094 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
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PA (GETH ) GENENTECH INC. 21.7%; Score 196.6; DB 10; Length 3719;
Query Match
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1345
ID ADE33646 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1346
ID ADD79698 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1347
ID ADD92735 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1348
ID ADE19155 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1349
ID ADE18603 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1350
ID ADE42799 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1351
ID ADD95588 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1352
ID ADE22474 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1353
ID ADD76592 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.

Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1354
ID ADE32542 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1355
ID ADE42234 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1356
ID ADD80250 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1357
ID ADD89278 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1358
ID ADE40562 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1359
ID ADE04361 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1360
ID ADE92490 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1361
ID ADG21199 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.7%; Score 196.6; DB 10; Length 3719;
RESULT 1362
ID ADG22840 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
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ID AD76234 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US200310087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1382
ID AD87598 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1383
ID AD86002 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1384
ID AD875450 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1385
ID AD83026 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1386
ID AD823578 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1387
ID AD824221 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1388
ID AD87046 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1389
ID AD88912 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1390
ID AD818051 standard; cDNA; 3719 BP.

DE Human PRO polynucleotide #25.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1391
ID AD88360 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1392
ID AD894380 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1393
ID AD890791 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1394
ID AD894932 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1395
ID AD893042 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1396
ID AD834623 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1397
ID AD891938 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1398
ID AD890239 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1399
ID AD89186 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.


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PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1400
ID ADG01965 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1401
ID ADG21751 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1402
ID ADG19821 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1403
ID ADP97727 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1404
ID ADG23944 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1405
ID ADP98298 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1406
ID ADG03129 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1407
ID ADP98850 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1408
ID ADG16435 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1409
ID ADG04894 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1410
ID ADG19161 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1411
ID ADG12998 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1412
ID ADG08055 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1413
ID ADG15225 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1414
ID ADP96623 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1415
ID ADG05808 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1416
ID ADG23392 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1417
ID ADG03681 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207423-A1.
PD 06-NOV-2003.
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PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1418
ID ADG54582 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1419
ID ADG06879 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1420
ID ADG07431 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1421
ID ADG54926 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1422
ID ADG60590 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1423
ID ADG61694 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1424
ID ADG81895 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1425
ID ADG57134 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1426
ID ADG56582 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1427
ID ADG55478 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1428
ID ADG58238 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1429
ID ADG70604 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1430
ID ADG57686 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1431
ID ADG53270 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1432
ID ADG71156 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1433
ID ADG81343 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1434
ID ADH30305 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1435
ID ADH11672 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;

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RESULT 1436
ID ADG52094 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1437
ID ADG53822 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1438
ID ADG80791 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1439
ID ADG56030 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1440
ID ADH12296 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1441
ID ADG61142 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1442
ID ADH28229 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1443
ID ADG54374 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1444
ID ADG59414 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1445
ID ADI80838 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1446
ID ADG09581 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1447
ID ADI15052 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1448
ID ADG08929 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1449
ID ADI14384 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1450
ID ADI17979 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1451
ID ADI63260 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1452
ID ADU77155 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1453
ID ADI65277 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1454
ID ADM27413 standard; cDNA; 3719 BP.
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DE cDNA encoding human PRO polypeptide #25.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1455
ID ADM12937 standard; cDNA; 3719 BP.
DE PRO4977 encoding sequence.
PN WO2004024077-A2.
PD 25-MAR-2004.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1456
ID ADM42137 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1457
ID ADM05275 standard; cDNA; 3719 BP.
DE Antiposrotatic cDNA sequence #857.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1458
ID ADM27999 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1459
ID ADI95481 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 13; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1460
ID ADI96033 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 13; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1461
ID ADRO7026 standard; cDNA; 3963 BP.
DE Full length human cDNA useful for treating neurological disease Seq 712.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.7%; Score 196.6; DB 13; Length 3963;
Best Local Similarity 80.2%; Pred. No. 9.9e-46;
RESULT 1462
ID ABA15615 standard; DNA; 4352 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11946.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 5; Length 4352;
Best Local Similarity 81.4%; Pred. No. 1e-45;
RESULT 1463
ID ACN89730 standard; DNA; 4619 BP.
DE Breast cancer related marker, seq id 10880.

PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILENNIUM PHARM INC.
Query Match 21.7%; Score 196.6; DB 11; Length 4619;
Best Local Similarity 82.7%; Pred. No. 1e-45;
RESULT 1464
ID ABA34825 standard; cDNA; 4713 BP.
DE Human mdt cDNA SEQ ID 386.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.7%; Score 196.6; DB 8; Length 4713;
Best Local Similarity 72.4%; Pred. No. 1.1e-45;
RESULT 1465
ID ACN39177 standard; cDNA; 4823 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325431, SEQ ID NO:3161.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GENH-) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 13; Length 4823;
Best Local Similarity 72.4%; Pred. No. 1.1e-45;
RESULT 1466
ID AAK67118 standard; DNA; 5744 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21930.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 5744;
Best Local Similarity 79.1%; Pred. No. 1.1e-45;
RESULT 1467
ID AAK66160 standard; DNA; 6153 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20972.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 6153;
Best Local Similarity 82.6%; Pred. No. 1.2e-45;
RESULT 1468
ID AAK69113 standard; DNA; 10553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23925.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 10553;
Best Local Similarity 76.9%; Pred. No. 1.4e-45;
RESULT 1469
ID ABA16395 standard; DNA; 10553 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8726.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 5; Length 10553;
Best Local Similarity 76.9%; Pred. No. 1.4e-45;
RESULT 1470
ID AAD14749 standard; DNA; 12394 BP.
DE Human glycogen synthase kinase 3 alpha genomic DNA.
PN WO200152865-A1.
PD 26-JUL-2001.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.7%; Score 196.6; DB 4; Length 12394;
Best Local Similarity 80.2%; Pred. No. 1.5e-45;
RESULT 1471
ID AAV05384 standard; DNA; 14237 BP.
DE Human cathepsin K gene.
PN WO9747642-A1.
PD 18-DEC-1997.
PA (SMIT-) SMITHKLINE BEECHAM CORP.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 2; Length 14237;
Best Local Similarity 81.8%; Pred. No. 1.6e-45;
RESULT 1472
ID AAU07092 standard; DNA; 14792 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 9780.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.6; DB 4; Length 14792;
 Best Local Similarity 75.1%; Pred. No. 1.6e-45;
 RESULT 1473
 ID AAV35616 standard; DNA; 15577 BP.
 DE SHOX gene preliminary nucleotide sequence (HOX93).
 PN WO9814568-A1.
 PD 09-APR-1998.
 PA (RAP/) RAPPOLD-HOERBRAND G.
 Query Match 21.7%; Score 196.6; DB 2; Length 15577;
 Best Local Similarity 82.6%; Pred. No. 1.7e-45;
 RESULT 1474
 ID AAL07093 standard; DNA; 16851 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9781.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.6; DB 4; Length 16851;
 Best Local Similarity 75.1%; Pred. No. 1.7e-45;
 RESULT 1475
 ID AAL07094 standard; DNA; 16853 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9782.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.6; DB 4; Length 16853;
 Best Local Similarity 75.1%; Pred. No. 1.7e-45;
 RESULT 1476
 ID AAD58283 standard; DNA; 18099 BP.
 DE Human tumour suppressor gene, lmt intron 4 DNA.
 PN WO200306869-A1.
 PD 14-AUG-2003.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 Query Match 21.7%; Score 196.6; DB 9; Length 18099;
 Best Local Similarity 83.1%; Pred. No. 1.8e-45;
 RESULT 1477
 ID ACN44570 standard; DNA; 19640 BP.
 DE Human genomic sequence hCG38237.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 11; Length 19640;
 Best Local Similarity 82.6%; Pred. No. 1.8e-45;
 RESULT 1478
 ID AAD56087 standard; DNA; 27184 BP.
 DE Human FOSB carcinoma associated (CA) gene.
 PN WO2003035837-A2.
 PD 01-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 8; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1479
 ID ADA02449 standard; DNA; 27184 BP.
 DE Human FOSB carcinoma associated gene, SEQ ID NO:968.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 9; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1480
 ID ADB72188 standard; DNA; 27184 BP.
 DE Human FOSB gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 10; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1481
 ID ADE82926 standard; DNA; 27184 BP.
 DE Human FOSB genomic DNA sequence.

PN WO2003080808-A2.
 PD 02-OCT-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 10; Length 27184;
 Best Local Similarity 80.2%; Pred. No. 2.1e-45;
 RESULT 1482
 ID AAV35620 standard; DNA; 32367 BP.
 DE Human SHOX (short stature homeobox containing gene) gene sequence.
 PN WO9814568-A1.
 PD 09-APR-1998.
 PA (RAP/) RAPPOLD-HOERBRAND G.
 Query Match 21.7%; Score 196.6; DB 2; Length 32367;
 Best Local Similarity 82.6%; Pred. No. 2.2e-45;
 RESULT 1483
 ID AAK73535 standard; DNA; 38358 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28347.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.6; DB 4; Length 38358;
 Best Local Similarity 80.2%; Pred. No. 2.4e-45;
 RESULT 1484
 ID ADQ97152 standard; DNA; 58651 BP.
 DE Human cancer associated sequence HD08-008, SEQ ID 128.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 58651;
 Best Local Similarity 82.9%; Pred. No. 2.8e-45;
 RESULT 1485
 ID ADQ97343 standard; DNA; 61739 BP.
 DE Human cancer associated sequence HD08-035, SEQ ID 320.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 61739;
 Best Local Similarity 78.1%; Pred. No. 2.8e-45;
 RESULT 1486
 ID AAD39317 standard; DNA; 62804 BP.
 DE Human calcium/calmodulin-dependent protein kinase genomic DNA.
 PN US6387677-B1.
 PD 14-MAY-2002.
 PA (PEKE) PE CORP NY.
 Query Match 21.7%; Score 196.6; DB 6; Length 62804;
 Best Local Similarity 70.6%; Pred. No. 2.9e-45;
 RESULT 1487
 ID ABX10916 standard; DNA; 62804 BP.
 DE Genomic DNA encoding novel human kinase.
 PN US2002132325-A1.
 PD 19-SEP-2002.
 PA (PEKE) PE CORP NY.
 Query Match 21.7%; Score 196.6; DB 8; Length 62804;
 Best Local Similarity 70.6%; Pred. No. 2.9e-45;
 RESULT 1488
 ID ADO52582 standard; DNA; 62804 BP.
 DE Human kinase genomic DNA.
 PN US2004101885-A1.
 PD 27-MAY-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 21.7%; Score 196.6; DB 12; Length 62804;
 Best Local Similarity 70.6%; Pred. No. 2.9e-45;
 RESULT 1489
 ID ACN44594 standard; DNA; 74234 BP.
 DE Human genomic sequence hCG15373.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.6; DB 11; Length 74234;
 Best Local Similarity 80.2%; Pred. No. 3.1e-45;
 RESULT 1490
 ID ADQ97278 standard; DNA; 86149 BP.
 DE Human cancer associated sequence HD08-025, SEQ ID 254.
 PN WO2004060304-A2.

PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.7%; Score 196.6; DB 12; Length 86149;
Best Local Similarity 82.6%; Pred. No. 3.2e-45;
RESULT 1491
ID ADP08387 standard; DNA: 94400 BP.
DE Human glycoprotein VI (platelet) (GP6/GPIV/GPII) genomic DNA.
Query Match 21.7%; Score 196.6; DB 12; Length 94400;
Best Local Similarity 82.6%; Pred. No. 3.3e-45;
RESULT 1492
ID ADC85367 standard; DNA: 96593 BP.
DE Mouse Bln coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 10; Length 96593;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1493
ID ADA02888 standard; DNA: 96594 BP.
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 9; Length 96594;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1494
ID ADB72626 standard; DNA: 96594 BP.
DE Human BLM gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 10; Length 96594;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1495
ID ADM74483 standard; DNA: 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 21.7%; Score 196.6; DB 12; Length 96594;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1496
ID MAD41740 standard; DNA: 99500 BP.
DE Human RECQL2 DNA #1.
PN US6399378-B1.
PD 04-JUN-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.7%; Score 196.6; DB 6; Length 99500;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1497
Query Match 21.7%; Score 196.6; DB 9; Length 110000;
Best Local Similarity 80.2%; Pred. No. 3.6e-45;
RESULT 1498
Query Match 21.7%; Score 196.6; DB 12; Length 110000;
Best Local Similarity 80.2%; Pred. No. 3.6e-45;
RESULT 1499
ID ABN9504 standard; DNA: 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.7%; Score 196.6; DB 6; Length 110096;
Best Local Similarity 79.1%; Pred. No. 3.6e-45;
RESULT 1500
ID ADQ18808 standard; DNA: 111084 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1627.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 196.6; DB 12; Length 111084;
Best Local Similarity 80.2%; Pred. No. 3.6e-45;

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